Search Paper 3

```
Trying 01180...Open

PLEASE ENTER HOST PORT ID:
PLEASE ENTER HOST PORT ID:x
LOGINID:d185jsb
PASSWORD:
TERMINAL (ENTER 1, 2, 3, 4, OR ?): 3


  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *                                                               *
  *           Welcome to MESSENGER (APS Text) at USPTO            *
  *                                                               *
  *                                                               *
  *    The USPTO production files are current through:            *
  *    APR 07 1998 for U.S. Patent Text Data.                     *
  *    APR 07 1998 for U.S. Current Classification data.          *
  *    APR 07 1998 for U.S. Patent Image Data.                    *
  *                                                               *
  *       * PLEASE USE 305-9000 FOR NEW TELEPHONE NUMBER *        *
  *                                                               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  * More U.S. patent data is now available on APS.  The new       *
  * USOCR file contains patents issued in 1970, plus some         *
  * patents that were missing from the USPAT file.  See the       *
  * Patents News Folder under the Public Folders in e-mail for    *
  * more information on using the new file.  Thank you.           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *  DISCLAIMER:                                                  *
  *  Neither the United States Government, nor any agency         *
  *  thereof, nor any of their contractors, subcontractors or     *
  *  employees make any warranty, expressed or implied,           *
  *  including any warranty of marketability of fitness for a     *
  *  particular purpose; nor assumes any legal liability or       *
  *  responsibility for any party's use, or the results of        *
  *  such, of the data.                                           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *                Help Desk --> 703-305-9000                     *
  *                                                               *
  *    The Help Desk is staffed for APS support 7 days/week.      *
  *      Monday through Friday:      6:30am - 9:00pm              *
  *      Saturday, Sunday, Holidays: 8:30am - 5:00 pm             *
  *                                                               *
  *    The Help Desk staff at this number will handle all APS     *
  *    related questions.                                         *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *    >>>>>>>>>>>>> NEW SUNDAY HOURS !!! <<<<<<<<<<<<<           *
  *                                                               *
  *    The APS is available:                                      *
  *            6:30am - 9:00pm Monday through Friday              *
  *            7:30am - 5:00pm Saturday, Sunday, Holidays         *
  *                                                               *
  *      APS is unavailable Thanksgiving Day, Christmas Day,      *
  *      and New Year's Day.                                      *
  *                                                               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
FILE 'USPAT' ENTERED AT 16:05:52 ON 13 APR 1998

  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *              W E L C O M E   T O   T H E                      *
```

```
  *        U. S.   P A T E N T   T E X T   F I L E           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

=> s pombe (p) ((ars) or autonomous?)

           370 POMBE
           980 ARS
          6351 AUTONOMOUS?
L1           9 POMBE (P) ((ARS) OR AUTONOMOUS?)

=> d 1-9 kwic
```

US PAT NO: 5,710,016 [IMAGE AVAILABLE] L1: 1 of 9

DETDESC:

DETD(95)

The . . . fragment ETANG Bam HI-Xho I of about 1.8 kbp. This fragment was inserted into an expression vector pREP1 for Schizosaccharomyces **pombe** [K. Maundrell et al., the Journal of Biological Chemistry, 265: 10857-10864 (1990)]. Plasmid pREP1 is a shuttle vector which contains an ampicillin resistant marker, a yeast resistant marker LEU2, a Schizosaccharomyces **pombe** **autonomous** replication sequence **ars**, and a promotor nmt 1 which is induced by lack of thiamine. After digestion of plasmid pREP1 by a restriction. . .

US PAT NO: 5,686,412 [IMAGE AVAILABLE] L1: 2 of 9

SUMMARY:

BSUM(19)

In . . . sequences and biological replicas thereof. Specifically illustrating the invention are Saccharomyces cerevisiae DNAs including those encoding HRR25 and NUF1, Schizosaccharomyces **pombe** DNAs including those encoding Hhp1+ and Hhp2+, and human DNAs including those encoding CKI.alpha.1Hu, CKI.alpha.2Hu, CKI.alpha.3Hu, CKI.gamma.1Hu, CKI.gamma.2Hu, and CKI.delta.Hu. Also provided are **autonomously** replicating recombinant constructions such as plasmid and viral DNA vectors incorporating such sequences and especially vectors wherein DNA encoding an. . .

US PAT NO: 5,663,061 [IMAGE AVAILABLE] L1: 3 of 9

SUMMARY:

BSUM(15)

Transformations of S. **pombe** with a plasmid (pDB248) were described for the first time by Beach and Nurse (Nature 290, (1981) pp 140-142). The vector constructed by them has an element which makes the plasmid capable of **autonomous** replication, but it emerged that this vector does not remain stably in the cells and is lost during mitotic segregation. Another vector (pFL20), which was developed by Losson and Lacroute (1983) Cell 32, 371-377, contains, in addition to the **ars** element, a DNA unit (stb) which results in the plasmid being passed on symmetrically to parent and daughter cell during. . .

DETDESC:

DETD(4)

The . . . vector pMB229 which was produced has the advantage over the plasmid pEVP11 that 1. it is able to undergo stable **autonomous** replication in S. **pombe**, 2. non-essential DNA regions, such as coding regions of the E. coli tetracycline gene and of the S. cerevisiae 2. . .

US PAT NO: 5,627,064 [IMAGE AVAILABLE] L1: 4 of 9

SUMMARY:

BSUM(20)

In . . . and biological replicas thereof. Specifically illustrating the invention are Saccharomyces cerevisiae DNAs including those encoding HRR25 and NUF 1, Schizosaccharomyces **pombe** DNAs including those encoding Hhp1+ and Hhp2+, and human DNAs including those encoding CKI.alpha.1Hu, CKI.alpha.2Hu, and CKI.alpha.3Hu. Also provided are **autonomously** replicating recombinant constructions such as plasmid and viral DNA vectors incorporating such sequences and especially vectors wherein DNA encoding an. . .

US PAT NO: 5,589,372 [IMAGE AVAILABLE] L1: 5 of 9

DETDESC:

DETD(121)

pDB20 (Fikes, et al. Nature 346:291 (1990)) is a high copy number, **autonomously** replicating Saccharomyces cerevisiae--Escherichia coli shuttle vector which confers ampicillin resistance to Escherichia coli and uracil prototrophy to ura3 yeast. It. . . contains a Saccharomyces cerevisiae ADH1 promoter fragment suitable for expression of heterologous cDNA's. Expression libraries bearing HeLa cell or Schizosaccharomyces **pombe** cDNAs were obtained from L. Guarente (Harvard University (Fikes, et al. Nature 346:291 (1990)); both contained polydT-primed cDNAs inserted at. . .

US PAT NO: 5,527,896 [IMAGE AVAILABLE] L1: 6 of 9

DETDESC:

DETD(66)

Plasmids pATG16 and pATG29 were selected by complementation in the S. **pombe** diploid strain SP565. This strain is homozygous for disruptions of ras1 (ras1::LEU2). As a consequence, this strain fails to sporulate. . . 29 and 30; and 31 and 32, respectively. These genes have unknown function The vector used for screening in S. **pombe** differs from the vector used for screening in S. cerevisiae. This vector, pAAUN-ATG, utilizes an S. **pombe** specific promoter, the adh promoter, and was constructed as follows. The cloning vector pAAUN was derived from plasmid pART1 (McLeod. . . EMBO J., 6:729-736 (1987) by replacing the S. cerevisiae LEU2 gene with a 1.8 kbp HindIII ura4 fragment from S. **pombe** and adding NotI linkers at the SmaI site of the polylinker (PL) derived from Viera et al., Methods in Enzymology, 153:3-11 (1987). pAAUN contains the S. **pombe** adh promter for gene expression and an **ARS**

region for DNA replidation. Plasmid pAAUN-ATG, was derived from plasmid pART8, obtained from David Beach, at Cold Spring Harbor Laboratory,. . .

US PAT NO: 5,443,962 [IMAGE AVAILABLE] L1: 7 of 9

DETDESC:

DETD(37)

The . . . vector, resulting in the pARTN-cdc25A construct harboring human cdc25A cDNA in sense orientation to the constitutive adh promoter. The S. **Pombe autonomously** replicating pARTN vector is derived from pART3 (McLeod et al. (1987) EMBO 6:729) by ligation of a NcoI linker (New. . .

US PAT NO: 5,441,880 [IMAGE AVAILABLE] L1: 8 of 9

DETDESC:

DETD(73)

To . . . do indeed encode proteins that are functionally related to fission yeast cdc25, the human genes were subcloned into the S. **pombe autonomously**-replicating expression vector, pARTN (carrying the LEU2 marker under the control of the constitutive alcohol dehydrogenase promoter, described in experimental procedures).. . .

US PAT NO: 5,270,201 [IMAGE AVAILABLE] L1: 9 of 9

SUMMARY:

BSUM(11)

At . . . isolated only from lower eukaryotic species. ARSs have been isolated from the unicellular fungi Saccharomyces cerevisiae (brewer's yeast) and Schizosaccharomyces **pombe** (see Stinchcomb et al., Nature 282:39- 43 (1979) and Hsiao et al., J. Proc. Natl. Acad. Sci. USA 76:3829-3833 (1979)). ARSs behave like replication origins allowing DNA molecules that contain the **ARS** to be replicated as an episome after introduction into the cell nuclei of these fungi. Although plasmids containing these sequences. . .

SUMMARY:

BSUM(22)

DNA . . . not promote extrachromosomal replication of these molecules in mouse cells (see Roth et al., Mol. Cell. Biol. 3:1898-1908 (1983)). An **ARS** sequenced from cultivated tomato, which operates in yeast, fails to function in tomato cells (see Zabel, P., "Toward the Construction. . . of the vertebrate Xenopus (Yu, et al., Gene 56:313 (1987)). Finally, although researchers were able to show that a S. **pombe** chromosome can replicate at a reduced efficiency in mouse cells, the centromeres of this lower eukaryote apparently do not function. . .

=> d 1-9 bib ab

```
  *        U. S.   P A T E N T   T E X T   F I L E           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

=> s cosmid (p) (yeast or pombe)

          1006 COSMID
           646 COSMIDS
          1308 COSMID
                 (COSMID OR COSMIDS)
         22124 YEAST
          4835 YEASTS
         23833 YEAST
                 (YEAST OR YEASTS)
           370 POMBE
L1         311 COSMID (P) (YEAST OR POMBE)

=> s cosmid (p) pombe

          1006 COSMID
           646 COSMIDS
          1308 COSMID
                 (COSMID OR COSMIDS)
           370 POMBE
L2           5 COSMID (P) POMBE

=> d 1-5 kwic
```

US PAT NO: 5,622,823 [IMAGE AVAILABLE] L2: 1 of 5

SUMMARY:

BSUM(10)

Lehrach's . . . Zehetner, G., Lennon, G. G., Douglas, C., Nizetic, D., Goodfellow, P. N., and Lehrach, H. (1991). Mapping irradiation hybrids to **cosmid** and yeast artificial chromosome libraries by direct hybridization of Alu-PCR products. Nucleic Acids Res, 19(12): 3315-3318). This group has noted. . . Lehrach, H. (1993). Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of Schizosaccharomyces **pombe**. Nucleic Acids Research, 21(8): 1965-1974). Studies of the distribution of Alu and L-1 interspersed repetitive sequences (IRS) in YACs (Arveiler,. . .

US PAT NO: 5,604,100 [IMAGE AVAILABLE] L2: 2 of 5

DETDESC:

DETD(101)

For . . . Boukhgalter, P. Zhang, M.-T. Yu, R. Rothstein, D. Warburton, I. S. Edelman, and A. Efstratiadis, "Assembly of ordered contigs of **cosmids** selected with YACs of human chromosome 13," Genomics, vol. 21, pp. 525-537, 1994; R. Mort, A. Grigoriev, E. Maier, J.. . . and H. Lehrach, "Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of Schizosaccharomyces **pombe**," Nucleic Acids Research, vol. 21, no. 8, pp. 1965-1974, 1993), incorporated by reference.

DETDESC:

DETD(188)

This . . . Boukhgalter, P. Zhang, M.-T. Yu, R. Rothstein, D. Warburton, I. S. Edelman, and A. Efstratiadis, "Assembly of ordered contigs of **cosmids** selected with YACs of human chromosome 13," Genomics, vol. 21, pp. 525-537, 1994; R. Mott, A. Grigoriev, E. Maier, J.. . . and H. Lehrach, "Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of Schizosaccharomyces **pombe**," Nucleic Acids Research, vol. 21, no. 8, pp. 1965-1974, 1993), incorporated by reference. With large variations in clone size, insert. . .

US PAT NO: 5,151,354 [IMAGE AVAILABLE] L2: 3 of 5

SUMMARY:

BSUM(18)

According to the present invention, in addition a shuttle **cosmid** vector has been constructed which can be used as a shuttle vector for transformation of Schwanniomyces, Saccharomyces, Escherichia coli and Schizosaccharomyces **pombe**.

US PAT NO: 5,100,794 [IMAGE AVAILABLE] L2: 4 of 5

SUMMARY:

BSUM(18)

According to the present invention, in addition a shuttle **cosmid** vector has been constructed which can be used as a shuttle vector for transformation of Schwanniomyces, Saccharomyces, Escherichia coli and Schizosaccharomyces **pombe**.

US PAT NO: 4,894,331 [IMAGE AVAILABLE] L2: 5 of 5

DETDESC:

DETD(41)

Moreover, . . . any of the following without limitation thereto: a phage vector [see e.g., Murray, et al., Nature, 251, 476 (1974)]; a **cosmid** vector [see e.g., Cattaneo, et al., Nucleic Acids Res., 9, 2777 (1981)]; a yeast plasmid [see e.g., Livingston, Genetics, 86,. . . 3, 637-642 (1985]. It is suggested in Schellenberg, et al., supra, for example, that because both Saccharomyces cerevisiae and Schizosaccharomyces **pombe** are xylose negative but are capable of fermenting xylose to ethanol, the cloning and expression of E. coli xylose isomerase. . .

=> d 3,4 bib ab

US PAT NO: 5,151,354 [IMAGE AVAILABLE] L2: 3 of 5
DATE ISSUED: Sep. 29, 1992
TITLE: Fermentation processes using amylolytic enzyme producing microorganisms
INVENTOR: Alexander Strasser, Chopinstr 7, Dusseldorf, Federal

Republic of Germany
Feodor B. Martens, Chopinstr 7, HE Leiden, Federal Republic of Germany
Jurgen Dohmen, Chopinstr 7, Meerbushl, Federal Republic of Germany
Cornelius P. Hollenberg, Chopinstr 7, D-4000 Dusseldorf, Federal Republic of Germany
ASSIGNEE: Cornelius Hollenberg, Dusseldorf, Federal Republic of Germany (foreign indiv.)
APPL-NO: 07/748,161
DATE FILED: Aug. 21, 1991
ART-UNIT: 185
PRIM-EXMR: Richard A. Schwartz
ASST-EXMR: Michelle Johnson
LEGAL-REP: Iver P. Cooper

US PAT NO: 5,151,354 [IMAGE AVAILABLE] L2: 3 of 5

ABSTRACT:
This invention provides a method for producing amylolytic enzymes by culturing a microorganism, having received as a result of recombinant DNA technology DNA sequences from a donor yeast comprising the coding sequences for the amylolytic enzymes wherein the host microorganism is capable of expressing said amylolytic enzymes. Furthermore, this invention provides microorganisms genetically engineered as to being able to produce and express the amylolytic enzymes, a vector containing the DNA sequences, coding for the amylolytic enzymes and the respective DNA sequences. The said host microorganisms are useful in the production of biomass and many fermentation processes, preferably in the production of special beers.

US PAT NO: 5,100,794 [IMAGE AVAILABLE] L2: 4 of 5
DATE ISSUED: Mar. 31, 1992
TITLE: Amylolytic enzymes producing microorganisms, constructed by recombinant DNA technology and their use for permentation processes
INVENTOR: Alexander Strasser, Zonser Str. 6, Dusseldorf, Federal Republic of Germany
Feodor B. Martens, Hogenwoerd 13, HE Leiden, Netherlands
Jurgen Dohmen, Bretonenstr 20, Meerbushi, Federal Republic of Germany
Cornelius P. Hollenberg, Chopinstr 7, Dusseldorf, Federal Republic of Germany
APPL-NO: 07/085,107
DATE FILED: Aug. 13, 1987
ART-UNIT: 185
PRIM-EXMR: Robin L. Teskin
LEGAL-REP: Iver P. Cooper

US PAT NO: 5,100,794 [IMAGE AVAILABLE] L2: 4 of 5

ABSTRACT:
The cloning of Schwanniomyces glucoamylase and alpha-amylase genes is taught. The genes are expressed in recombinant host cells.

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y

U.S. Patent & Trademark Office LOGOFF AT 15:53:16 ON 13 APR 1998

Search Page 3

```
Trying 9351006...Open

Welcome to STN International!  Enter x:x
LOGINID:ssspta1805jxb
PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1  Feb  2  Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Mar 24  STN Express 4.1 with Discover! for Windows Now
                  Available
 NEWS  3  Mar 31  Free Connect Hour in KKF in April 1998
 NEWS  4  Apr 10  Derwent World Patents Index (DWPI) Coverage Expanded
                  to Include Mexico

 NEWS EXPRESS  Discover! is Year 2000 Compliant
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
  agreement.  Please note that this agreement limits use to scientific
  research.  Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

* * * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:05:48 ON 13 APR 1998

=> file medline, biosis

COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.15       0.15

FILE 'MEDLINE' ENTERED AT 11:05:59 ON 13 APR 1998

FILE 'BIOSIS' ENTERED AT 11:05:59 ON 13 APR 1998
COPYRIGHT (C) 1998 BIOSIS(R)

=> s cosmid and (yeast or schizosaccharomyces)

L1          918 COSMID AND (YEAST OR SCHIZOSACCHAROMYCES)

=> s l1 and vector

L2          102 L1 AND VECTOR

=> s l2 and pombe

L3            2 L2 AND POMBE
```

=> d 1-2 bib ab

L3 ANSWER 1 OF 2 MEDLINE
AN 93255209 MEDLINE
DN 93255209
TI Genome mapping of **Schizosaccharomyces pombe**.
AU Mizukami T; Garkavtsev I; Beach D; Marr T; Niwa O; Yanagida M
CS Tokyo Research Laboratories, Kyowa Hakko Kogyo Co., Ltd., Japan..
SO TANPAKUSHITSU KAKUSAN KOSO. PROTEIN, NUCLEIC ACID, ENZYME, (1993 Feb) 38 (3) 677-84. Ref: 16
Journal code: Q7D. ISSN: 0039-9450.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LA Japanese
EM 199308

L3 ANSWER 2 OF 2 MEDLINE
AN 93241164 MEDLINE
DN 93241164
TI Cloning and analysis of the mating type genes from Cochliobolus heterostrophus.
AU Turgeon B G; Bohlmann H; Ciuffetti L M; Christiansen S K; Yang G; Schafer W; Yoder O C
CS Department of Plant Pathology, Cornell University, Ithaca NY 14853..
SO MOLECULAR AND GENERAL GENETICS, (1993 Apr) 238 (1-2) 270-84.
Journal code: NGP. ISSN: 0026-8925.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X68399; GENBANK-X68398
EM 199307
AB Cochliobolus heterostrophus, a heterothallic Ascomycete, has a single mating type locus with two alternate forms called MAT-1 and MAT-2. MAT-1 was cloned by complementing a MAT-2 strain using a **cosmid** library from a MAT-1 strain and screening for a homothallic transformant. The **cosmid** recovered from this transformant was able to re-transform a MAT-2 strain to homothallism and MAT identity was proven by restriction fragment length polymorphism and conventional genetic mapping. All homothallic transformants could mate with either MAT-1 or MAT-2 strains, although the number of ascospores produced by self matings or crosses to MAT-2 strains was low. Progeny of selfed homothallic transformants were themselves homothallic. MAT-2 was cloned by probing a **cosmid** library from a MAT-2 strain with a fragment of insert DNA from a MAT-1 **cosmid**. A 1.5 kb subclone of either MAT-containing **cosmid** was sufficient to confer mating function in transformants. Examination of the DNA sequence of these subclones revealed that MAT-1 and MAT-2 contain 1297 bp and 1171 bp, respectively, of completely dissimilar DNA flanked by DNA common to both mating types. Putative introns were found (one in each MAT gene) which, when spliced out, would yield open reading frames (ORFs) that occupied approximately 90% of the dissimilar DNA sequences. Translation of the MAT-1 ORF revealed similarity to the Neurospora crassa MATA, Podospora anserina mat-, and Saccharomyces cerevisiae MAT alpha 1 proteins; translation of the MAT-2 ORF revealed similarity to the N. crassa MATa, P. anserina

mat+, and **Schizosaccharomyces pombe** mat-Mc
proteins. These gene products are all proven or proposed DNA binding proteins. Those with similarity to MAT-2 are members of the high mobility group.

```
=> d his

     (FILE 'HOME' ENTERED AT 11:05:48 ON 13 APR 1998)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 11:05:59 ON 13 APR 1998
L1           918 S COSMID AND (YEAST OR SCHIZOSACCHAROMYCES)
L2           102 S L1 AND VECTOR
L3             2 S L2 AND POMBE

=> s l2 and (ars or autonomously replicating sequence)

L4             0 L2 AND (ARS OR AUTONOMOUSLY REPLICATING SEQUENCE)

=> s cosmid and ((ars) or (autonomous?))

L5            43 COSMID AND ((ARS) OR (AUTONOMOUS?))

=> duplicate remove l5

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n

PROCESSING COMPLETED FOR L5
L6            26 DUPLICATE REMOVE L5 (17 DUPLICATES REMOVED)

=> d 1-26 bib ab


L6   ANSWER 1 OF 26  MEDLINE                                  DUPLICATE 1
AN   97245294     MEDLINE
DN   97245294
TI   Sequence analysis of a 37.6 kbp cosmid clone from the
     right arm of Saccharomyces cerevisiae chromosome XII, carrying YAP3,
     HOG1, SNR6, tRNA-Arg3 and 23 new open reading frames, among which
     several homologies to proteins involved in cell division control and
     to mammalian growth factors and other animal proteins are found.
AU   Verhasselt P; Volckaert G
CS   Katholieke Universiteit Leuven, Laboratory of Gene Technology,
     Belgium.
SO   YEAST, (1997 Mar 15) 13 (3) 241-50.
     Journal code: YEA. ISSN: 0749-503X.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
OS   GENBANK-A32646; GENBANK-B32646; GENBANK-D10017; GENBANK-L06279;
     GENBANK-S20150; GENBANK-T37940; GENBANK-U00043; GENBANK-X85802;
     GENBANK-X89154; GENBANK-Z47047; GENBANK-Z48179
EM   199708
AB   The nucleotide sequence of 37,639 bp of the right arm of chromosome
     XII has been determined. Twenty-five open reading frames (ORFs)
     longer than 300 bp were detected, two of which extend into the
     flanking cosmids. Only two (L2931 and L2961) of the 25
     ORFs correspond to previously sequenced genes (HOG1 and YAP3,
```

respectively). Another ORF is distinct from YAP3 but shows pronounced similarity to it. About half of the remaining ORFs show similarity to other genes or display characteristic protein signatures. In particular, ORF L2952 has striking homology with the probable cell cycle control protein crn of Drosophila melanogaster. L2949 has significant similarity to the human ZFM1 (related to a potential suppressor oncogene) and mouse CW17R genes, though it lacks the carboxy-terminal oligoproline and oligoglutamine stretches encoded by these mammalian genes. The small ORF L2922 is similar to part of the much larger yeast flocculation gene FLO1. Other sequences found in the 37639 bp fragment are one delta and one solo-sigma element, the tRNA-Arg3 gene, the small nuclear RNA gene SNR6 and three **ARS** consensus sequences.

L6 ANSWER 2 OF 26 MEDLINE DUPLICATE 2
AN 97197984 MEDLINE
DN 97197984
TI The sequence of 32b on the left arm of yeast chromosome XII reveals six known genes, a new member of the seripauperins family and a new ABS transporter homologous to the human multidrug resistance protein.
AU Purnelle B; Goffeau A
CS Unite de Biochimie Physiologique, Universite Catholique de Louvain, Louvain-la-Neuve, Belgium.
SO YEAST, (1997 Feb) 13 (2) 183-8.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X97560
EM 199707
EW 19970703
AB The analysis of a 32 kb DNA fragment from **cosmid** 2G12 on the left arm of chromosome XII identifies 14 open reading frames (ORFs) numbered L0948 to L1325, a new tRNA for proline, a delta remnant and two putative **ARS**. Six ORFs have been previously identified: HSP104, SSA2, SPA2, KNS1, DPS1/APS and SDC25. Three putative ORFs have significant homology with known proteins: L0968 is a new member of the very large 'seripauperins' family, comprising at least 20 yeast members; L1313 is a new ABC transporter highly homologous to the yeast cadmium resistance protein Ycf1p and to the human multidrug resistance protein hMRP1; the C-terminal part of L1325 present in our sequence is very homologous to the fruit fly abdominal segment formation protein Pumilio. Finally, two ORFs, L1201 and L1205, have weak homology with two yeast hypothetical proteins of unknown function identified by the yeast systematic sequencing genome. Since our nucleotide sequence overlaps by 11.6 kb the **cosmid** 2B18 sequenced by Miosga and Zimmerman (1996) on the right end, we have not reported here the analysis of the ORFs L1313, L1321 and L1325.

L6 ANSWER 3 OF 26 MEDLINE DUPLICATE 3
AN 96400916 MEDLINE
DN 96400916
TI Mosaic analysis using a ncl-1 (+) extrachromosomal array reveals that lin-31 acts in the Pn.p cells during Caenorhabditis elegans vulval development.
AU Miller L M; Waring D A; Kim S K
CS Department of Developmental Biology, Stanford University Medical

Center, California 94305, USA.
SO GENETICS, (1996 Jul) 143 (3) 1181-91.
Journal code: FNH. ISSN: 0016-6731.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199704
EW 19970402
AB We describe a genetic mosaic analysis procedure in which Caenorhabditis elegans mosaics are generated by spontaneous loss of an extrachromosomal array. This technique allows almost any C. elegans gene that can be used in germline transformation experiments to be used in mosaic analysis experiments. We identified a **cosmid** clone that rescues the mutant phenotype of ncl-1, so that this cell-**autonomous** marker could be used to analyze mosaic animals. To determine the sites of action for unc-29 and lin-31, an extrachromosomal array was constructed containing the ncl-1(+) **cosmid** linked to lin-31(+) and unc-29(+) **cosmids**. This array is mitotically unstable and can be lost to produce a clone of mutant cells. The specific cell division at which the extrachromosomal array had been lost was deduced by scoring the Ncl phenotypes of individual cells in genetic mosaics. The Unc-29 and Lin-31 phenotypes were then scored in these animals to determine in which cells these genes are required. This analysis showed that unc-29, which encodes a subunit of the acetylcholine receptor, acts in the body muscle cells. Furthermore, lin-31, which specifies cell fates during vulval induction and encodes a putative transcription factor similar to HNF-3/fork head, acts in the Pn.p cells.

L6 ANSWER 4 OF 26 BIOSIS COPYRIGHT 1998 BIOSIS
AN 97:273627 BIOSIS
DN 99565345
TI Essential features of vectors used for molecular cloning of eukaryotic genes.
AU Gupta S; Jain S K
CS Dep. Biochem., Hamdard Univ., Hamdard Nagar, New Delhi-110062, India
SO Proceedings of the National Academy of Sciences India Section B (Biological Sciences) 66 (3). 1996. 207-226. ISSN: 0369-8211
LA English
AB An ideal vector for cloning must be distinguishable from the host genome and should contain (i) an **autonomous** origin of replication, (ii) a region which is non-essential for its replication where the foreign DNA can be inserted, (iii) one or more selectable marker(s) such as resistance of antibiotics or certain autotrophic markers, which help to differentiate between wild type and recombinant molecules and (iv) unique restriction site(s) preferably within the marker gene, for the insertion of foreign gene(s), so that the recombination leads to marker inactivation.

L6 ANSWER 5 OF 26 MEDLINE DUPLICATE 4
AN 97075915 MEDLINE
DN 97075915
TI New **cosmid** vectors for library construction, chromosome walking and restriction mapping in filamentous fungi.
AU An Z; Farman M L; Budde A; Taura S; Leong S A
CS Department of Plant Pathology, University of Wisconsin, Madison 53706, USA.
NC GM33716 (NIGMS)

SO GENE, (1996 Oct 17) 176 (1-2) 93-6.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L76273
EM 199703
AB New **cosmid** vectors were constructed for the ascomycete fungus, Magnaporthe grisea and the basidiomycete fungus, Ustilago maydis. These vectors are capable of transforming M. grisea at frequencies of up to 5 transformants/micrograms linear DNA and U. maydis at up to 25 transformants/microgram circular DNA for integrative transformation. In addition, 2800 transformants/microgram DNA are possible when using an **autonomously** replicating vector. Since the promoters used in these vectors function in other ascomycete and basidiomycete fungi, we anticipate that these vectors will be widely applicable.

L6 ANSWER 6 OF 26 MEDLINE DUPLICATE 5
AN 95349579 MEDLINE
DN 95349579
TI Identification of an origin of bidirectional DNA replication in the ubiquitously expressed mammalian CAD gene.
AU Kelly R E; DeRose M L; Draper B W; Wahl G M
CS Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, California 92037, USA.
NC CA521416 (NCI)
GM521511 (NIGMS)
GM12957 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, (1995 Aug) 15 (8) 4136-48.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199511
AB Most DNA replication origins in eukaryotes localize to nontranscribed regions, and there are no reports of origins within constitutively expressed genes. This observation has led to the proposal that there may be an incompatibility between origin function and location within a ubiquitously expressed gene. The biochemical and functional evidence presented here demonstrates that an origin of bidirectional replication (OBR) resides within the constitutively expressed housekeeping gene CAD, which encodes the first three reactions of de novo uridine biosynthesis (carbamoyl-phosphate synthetase, aspartate carbamoyltransferase, and dihydroorotase). The OBR was localized to a 5-kb region near the center of the Syrian hamster CAD transcriptional unit. DNA replication initiates within this region in the single-copy CAD gene in Syrian baby hamster kidney cells and in the large chromosomal amplicons that were generated after selection with N-phosphonacetyl-L-aspartate, a specific inhibitor of CAD. DNA synthesis also initiates within this OBR in **autonomously** replicating extrachromosomal amplicons (CAD episomes) located in an N-phosphonacetyl-L-aspartate-resistant clone (5P20) of CHOK1 cells. CAD episomes consist entirely of a multimer of Syrian hamster CAD **cosmid** sequences (cCAD1). These data limit the functional unit of replication initiation and timing control to the 42 kb of Syrian hamster sequences contained in cCAD1. In addition, the data

transformant by transforming Escherichia coli with total genomic DNA of this transformant. Gene disruption and genetic analysis was carried out to prove that the previously unknown A. niger nicB gene had been cloned.

L6 ANSWER 11 OF 26 MEDLINE DUPLICATE 7
AN 94215890 MEDLINE
DN 94215890
TI Double-origin vectors for isolating bidirectional deletions useful in DNA sequence analysis.
AU Ahmed A
CS Department of Genetics, University of Alberta, Edmonton, Canada..
SO GENE, (1994 Apr 8) 141 (1) 71-3.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U03460; GENBANK-U03463; GENBANK-U03461
EM 199407
AB **Cosmids** containing two compatible origins of replication (oris) have been constructed for isolating bidirectional deletions in cloned DNA. The inserted fragment and the cos site are cut, respectively, with a restriction enzyme and lambda terminase to produce two linear fragments that are circularized to produce two **autonomously** replicating plasmids. Each plasmid contains a different portion of the insert fused to the cosL or cosR sequence. From a series of such deletion-bearing plasmids, the nucleotide sequence of the insert can be determined in both directions using cosL and cosR primers.

L6 ANSWER 12 OF 26 MEDLINE
AN 93233658 MEDLINE
DN 93233658
TI Localization of a bidirectional DNA replication origin in the native locus and in episomally amplified murine adenosine deaminase loci.
AU Carroll S M; DeRose M L; Kolman J L; Nonet G H; Kelly R E; Wahl G M
CS Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, California 92037..
NC GM27754 (NIGMS)
CA 48405 (NCI)
GM 12957 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, (1993 May) 13 (5) 2971-81.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199307
AB Gene amplification is frequently mediated by the initial production of acentric, **autonomously** replicating extrachromosomal elements. The 4,000 extrachromosomal copies of the mouse adenosine deaminase (ADA) amplicon in B-1/50 cells initiate their replication remarkably synchronously in early S phase and at approximately the same time as the single-copy chromosomal locus from which they were derived. The abundance of ADA sequences and favorable replication timing characteristics in this system led us to determine whether DNA replication initiates in ADA episomes within a preferred region and whether this region is the same as that used at the corresponding chromosomal locus prior to amplification. This study

reports the detection and localization of a discrete set of DNA fragments in the ADA amplicon which label soon after release of synchronized B-1/50 cells into S phase. A switch in template strand complementarity of Okazaki fragments, indicative of the initiation of bidirectional DNA replication, was found to lie within the same region. This putative replication origin is located approximately 28.5 kbp upstream of the 5' end of the ADA gene. The same region initiated DNA replication in the single-copy ADA locus of the parental cells. These analyses provide the first evidence that the replication of episomal intermediates involved in gene amplification initiates within a preferred region and that the same region is used to initiate DNA synthesis within the native locus.

L6 ANSWER 13 OF 26 MEDLINE DUPLICATE 8
AN 94123978 MEDLINE
DN 94123978
TI Unusual mitochondrial genome organization in cytoplasmic male sterile common bean and the nature of cytoplasmic reversion to fertility.
AU Janska H; Mackenzie S A
CS Department of Agronomy, Purdue University, West Lafayette, Indiana 47907..
SO GENETICS, (1993 Nov) 135 (3) 869-79.
Journal code: FNH. ISSN: 0016-6731.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199405
AB Spontaneous reversion to pollen fertility and fertility restoration by the nuclear gene Fr in cytoplasmic male sterile common bean (Phaseolus vulgaris L.) are associated with the loss of a large portion of the mitochondrial genome. To understand better the molecular events responsible for this DNA loss, we have constructed a physical map of the mitochondrial genome of a stable fertile revertant line, WPR-3, and the cytoplasmic male sterile line (CMS-Sprite) from which it was derived. This involved a **cosmid** clone walking strategy with comparative DNA gel blot hybridizations. Mapping data suggested that the simplest model for the structure of the CMS-Sprite genome consists of three **autonomous** chromosomes differing only in short, unique regions. The unique region contained on one of these chromosomes is the male sterility-associated 3-kb sequence designated pvs. Based on genomic environments surrounding repeated sequences, we predict that chromosomes can undergo intra- and intermolecular recombination. The mitochondrial genome of the revertant line appeared to contain only two of the three chromosomes; the region containing the pvs sequence was absent. Therefore, the process of spontaneous cytoplasmic reversion to fertility likely involves the disappearance of an entire mitochondrial chromosome. This model is supported by the fact that we detected no evidence of recombination, excision or deletion events within the revertant genome that could account for the loss of a large segment of mitochondrial DNA.

L6 ANSWER 14 OF 26 MEDLINE DUPLICATE 9
AN 93015637 MEDLINE
DN 93015637
TI A conjugation procedure for Bdellovibrio bacteriovorus and its use to identify DNA sequences that enhance the plaque-forming ability of a spontaneous host-independent mutant.

AU Cotter T W; Thomashow M F
CS Department of Microbiology, Michigan State University, East Lansing 48824..
SO JOURNAL OF BACTERIOLOGY, (1992 Oct) 174 (19) 6011-7.
Journal code: HH3. ISSN: 0021-9193.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199301
AB Wild-type bdellovibrios are obligate intraperiplasmic parasites of other gram-negative bacteria. However, spontaneous mutants that can be cultured in the absence of host cells occur at a frequency of 10(-6) to 10(-7). Such host-independent (H-I) mutants generally display diminished intraperiplasmic-growth capabilities and form plaques that are smaller and more turbid than those formed by wild-type strains on lawns of host cells. An analysis of the gene(s) responsible for the H-I phenotype should provide significant insight into the nature of Bdellovibrio host dependence. Toward this end, a conjugation procedure to transfer both IncQ and IncP vectors from Escherichia coli to Bdellovibrio bacteriovorus was developed. It was found that IncQ-type plasmids were capable of **autonomous** replication in B. bacteriovorus, while IncP derivatives were not. However, IncP plasmids could be maintained in B. bacteriovorus via homologous recombination through cloned B. bacteriovorus DNA sequences. It was also found that genomic libraries of wild-type B. bacteriovorus 109J DNA constructed in the IncP **cosmid** pVK100 were stably maintained in E. coli; those constructed in the IncQ **cosmid** pBM33 were unstable. Finally, we used the conjugation procedure and the B. bacteriovorus libraries to identify a 5.6-kb BamHI fragment of wild-type B. bacteriovorus DNA that significantly enhanced the plaque-forming ability of an H-I mutant, B. bacteriovorus BB5.

L6 ANSWER 15 OF 26 MEDLINE DUPLICATE 10
AN 92331948 MEDLINE
DN 92331948
TI Plasmid cloning vectors for the conjugal transfer of DNA from Escherichia coli to Streptomyces spp.
AU Bierman M; Logan R; O'Brien K; Seno E T; Rao R N; Schoner B E
CS Lilly Research Laboratories, A Division of Eli Lilly and Company, Indianapolis, IN 46285-0424..
SO GENE, (1992 Jul 1) 116 (1) 43-9.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199210
AB We have constructed cloning vectors for the conjugal transfer of DNA from Escherichia coli to Streptomyces spp. All vectors contain the 760-bp oriT fragment from the IncP plasmid, RK2. Transfer functions need to be supplied in trans by the E. coli donor strain. We have incorporated into these vectors selectable antibiotic-resistance markers (AmR, ThR, SpR) that function in Streptomyces spp. and other features that should allow for: (i) integration via homologous recombination between cloned DNA and the Streptomyces spp. chromosome, (ii) **autonomous** replication, or (iii) site-specific integration at the bacteriophage phi C31 attachment site. Shuttle **cosmids** for constructing genomic libraries

and bacteriophage P1 cloning vector capable of accepting approx. 100-kb fragments are also described. A simple mating procedure has been developed for the conjugal transfer of these vectors from E. coli to Streptomyces spp. that involves plating of the donor strain and either germinated spores or mycelial fragments of the recipient strain. We have shown that several of these vectors can be introduced into Streptomyces fradiae, a strain that is notoriously difficult to transform by PEG-mediated protoplast transformation.

L6 ANSWER 16 OF 26 MEDLINE DUPLICATE 11
AN 91156718 MEDLINE
DN 91156718
TI Canonical ordered **cosmid** library of the symbiotic plasmid of Rhizobium species NGR234.
AU Perret X; Broughton W J; Brenner S
CS Laboratoire de Biologie Moleculaire des Plantes Superieures, Universite de Gen`eve, Switzerland..
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1991 Mar 1) 88 (5) 1923-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199106
AB Many of the bacterial genes involved in nodulation (nod) and nitrogen fixation (nif) are dispersed over the 500-kilobase plasmid pNGR234a of the broad host-range Rhizobium species NGR234. As a first step toward generating a complete physical and genetic map of the plasmid, a full overlapping collection of **cosmids** was derived from a total genomic library. Clones were aligned by combining fingerprinting, hybridization, and pulsed-field gel electrophoresis data. Symbiotic loci were localized by probing a representative set of **cosmids** with both homologous and heterologous genes. nodABC, nodD1, nodD2, nodSU, nolB, and region II are widely dispersed over pNGR234a, while the two functional copies of nifKDH are separated by only 28 kilobases. Interestingly, sequences homologous to nodE, nodG, nodP, and nodQ have been assigned to another **autonomously** replicating element in Rhizobium species NGR234. Similarly one copy of the structural dctA gene is located on the symbiotic plasmid (dctA1) while the other is on what we assume to be the chromosome.

L6 ANSWER 17 OF 26 MEDLINE DUPLICATE 12
AN 90377210 MEDLINE
DN 90377210
TI Molecular cloning and analysis of the scon-2 negative regulatory gene of Neurospora crassa.
AU Paietta J V
CS Department of Biochemistry, Wright State University, Dayton, Ohio 45435..
NC GM-38671 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, (1990 Oct) 10 (10) 5207-14.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199012
AB The sulfur regulatory system of Neurospora crassa is composed of a

group of highly regulated structural genes (e.g., the gene encoding arylsulfatase) that are under coordinate control of scon+ (sulfur controller) negative and cys-3+ positive regulatory genes. In scon-1 (previously designated sconC) and scon-2 mutants, there is constitutive expression of sulfur structural genes regardless of the sulfur level available to the cells. The scon-2+ gene was cloned by sib selection screening of a **cosmid**-based gene library. The screening was based on the use of chromate, a toxic sulfate analog, which is transported into scon-2 cells grown on high sulfur but is not transported into cells that have regained normal sulfur regulation. Restriction fragment length polymorphism analysis was used to confirm that the cloned segment mapped to the proper chromosomal location. In wild-type cells, Northern (RNA) blot analysis showed that a 2.6-kilobase scon-2+ transcript was present at a substantial level only under sulfur-derepressing conditions. Kinetic analysis showed that scon-2+ mRNA content increased as the cells became sulfur starved. Further, scon-2+ RNA was detectable in a nuclear transcription assay only under derepressing conditions. In scon-1, the levels of scon-2+ mRNA were found to be constitutive. In the cys-3 regulatory mutant, there was a reduced level of scon-2+ transcript. cys-3+ and **ars**-1+ mRNAs were present under both derepressing and repressing conditions in the scon-2 mutant. Repeat-induced point mutation-generated scon-2 mutants were identical in phenotype to the known mutant.

L6 ANSWER 18 OF 26 MEDLINE DUPLICATE 13
AN 89172067 MEDLINE
DN 89172067
TI Transposed human immunoglobulin V kappa gene regions carry clusters of conserved sequence elements.
AU Lotscher E; Siwka W; Zimmer F J; Grummt F; Zachau H G
CS Institut fur Physiologische Chemie, Universitat Munchen, F.R.G..
SO GENE, (1988 Sep 30) 69 (2) 225-36.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK; GENBANK-M20808; GENBANK-M20809; GENBANK-M20810; GENBANK-M20811; GENBANK-M20812; GENBANK-M20813
EM 198907
AB The V kappa I gene regions which have been transposed in evolution from the site of the kappa locus on chromosome 2 to chromosomes 1, 22, and other chromosomes, are very similar and may have been derived from one ancestor gene. Upstream from the transposed genes (called orphons) two types of conserved sequence elements were found using a mouse cell assay system. One type is homologous to the murine sequences which were previously thought to be **ARS** elements; the other one is related to the binding site of the replication/transcription factor NFIII. Such a combination of elements was seen neither in hybridization experiments with the 1 Mb of the kappa locus available on **cosmid** clones nor in a computer-aided search of sequence data libraries. We speculate that in the evolutionary past, the clustered elements played a role in the transposition of the V kappa genes, perhaps by causing an over-replication and/or by facilitating the integration of the genes.

L6 ANSWER 19 OF 26 MEDLINE
AN 88041150 MEDLINE

DN 88041150
TI Transformation of Paramecium by microinjection of a cloned serotype gene.
AU Godiska R; Aufderheide K J; Gilley D; Hendrie P; Fitzwater T; Preer L B; Polisky B; Preer J R Jr
CS Department of Biology, Indiana University, Bloomington 47405.
NC GM31745 (NIGMS)
GM24212 (NIGMS)
GM34681 (NIGMS)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1987 Nov) 84 (21) 7590-4.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 198802
AB Paramecia of a given serotype express only one of several possible surface proteins called immobilization antigens (i-antigens). A 16-kilobase plasmid containing the gene for immobilization antigen A from Paramecium tetraurelia, stock 51, was injected into the macronucleus of deletion mutant d12, which lacks that gene. Approximately 40% of the injected cells acquired the ability to express serotype A at 34 degrees C. Expression appeared to be regulated normally. The transformed cells, like wild type, could be switched to serotype B by antiserum treatment and culture at 19 degrees C; on transfer to 34 degrees C, they switched back to serotype A expression. Many of the lines retained the ability to express serotype A until autogamy, when the old macronucleus is replaced by a new one derived from the micronucleus. DNA from transformants contained the injected plasmid sequences, which were replicated within the paramecia. No evidence for integration was obtained. The majority of replicated plasmid DNA comigrated with a linearized form of the input plasmid. Nonetheless, the pattern of restriction fragments generated by transformant DNA and that generated by input plasmid DNA are identical and consistent with a circular rather than a linear map. These conflicting observations can be reconciled by assuming that a mixture of different linear fragments is present in the transformants, each derived from the circular plasmid by breakage at a different point. Copy-number determinations suggest the presence of 45,000-135,000 copies of the injected plasmid per transformed cell. These results suggest that the injected DNA contains information sufficient for both controlled expression and **autonomous** replication in Paramecium.

L6 ANSWER 20 OF 26 MEDLINE DUPLICATE 14
AN 87257873 MEDLINE
DN 87257873
TI Characterization of an episome produced in hamster cells that amplify a transfected CAD gene at high frequency: functional evidence for a mammalian replication origin.
AU Carroll S M; Gaudray P; De Rose M L; Emery J F; Meinkoth J L; Nakkim E; Subler M; Von Hoff D D; Wahl G M
NC GM27754 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, (1987 May) 7 (5) 1740-50.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 198710
AB In a previous study (G. M. Wahl, B. Robert de Saint Vincent, and M. L. De Rose, Nature (London) 307:516-520, 1984), we used gene transfer of a CAD **cosmid** to demonstrate that gene position profoundly affects amplification frequency. One transformant, T5, amplified the donated CAD genes at a frequency at least 100-fold higher than did the other transformants analyzed. The CAD genes in T5 and two drug-resistant derivatives were chromosomally located. In this report, we show that a subclone of T5 gives rise to an extrachromosomal molecule (CAD episome) containing the donated CAD genes. Gel electrophoresis indicated that the CAD episome is approximately 250 to 300 kilobase pairs, and a variety of methods showed that it is a covalently closed circle. We show that the CAD episome replicates semiconservatively and approximately once per cell cycle. Since the CAD **cosmid**, which comprises most of the CAD episome, does not replicate **autonomously** when transfected into cells, our results indicate that either the process which generated the episome resulted in a cellular origin of DNA replication being linked to the CAD sequences or specific rearrangements within the episome generated a functional origin. The implications of these results for mechanisms of gene amplification and the genesis of minute chromosomes are discussed.

L6 ANSWER 21 OF 26 MEDLINE DUPLICATE 15
AN 87218488 MEDLINE
DN 87218488
TI Expression and rescuing of a cloned human tumour necrosis factor gene using an EBV-based shuttle **cosmid** vector.
AU Kioussis D; Wilson F; Daniels C; Leveton C; Taverne J; Playfair J H
SO EMBO JOURNAL, (1987 Feb) 6 (2) 355-61.
Journal code: EMB. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198709
AB A **cosmid** vector carrying the Epstein-Barr virus origin of replication, the EBNA-1 gene, the hygromycin phosphotransferase (hph) gene and pBR322 sequences has been constructed. This **cosmid** can replicate **autonomously** in the nucleus of human tissue culture cells, even when it carries a 35-kb long insert. The **cosmid** can be rescued from the transfected cells by cloning it directly into ampicillin-sensitive Escherichia coli. A gene for human tumour necrosis factor (TNF) cloned into this **cosmid** vector was introduced in tissue culture cells, where it was transcribed into mature mRNA.

L6 ANSWER 22 OF 26 BIOSIS COPYRIGHT 1998 BIOSIS
AN 87:167138 BIOSIS
DN BA83:85579
TI CHARACTERIZATION AND SEQUENCE DETERMINATION OF THE REPLICATOR REGION IN THE HAIRY-ROOT-INDUCING PLASMID PRIA-4B.
AU NISHIGUCHI R; TAKANAMI M; OKA A
CS LAB. MOLECULAR BIOL., INST. CHEMICAL RES., KYOTO UNIV., UJI-SHI, KYOTO-FU 611, JPN.
SO MOL GEN GENET 206 (1). 1987. 1-8. CODEN: MGGEAE ISSN: 0026-8925
LA English
AB Starting from a **cosmid** library of the 250 kb hairy root inducing plasmid pRiA4b, a mini-pRiA4b replicon of 4.6 kb was isolated. This mini-plasmid was stably maintained in Agrobacterium

species and its replication characteristics, such as temperature-sensitive replication, copy number and incompatibility, were similar to those of the parental pRiA4b. Analysis of deletion mutants indicated that almost the entire 4.6 kb region was required for **autonomous** replication. The nucleotide sequence of mini-pRiA4b was determined by the chain-termination method. Three large open reading frames, which are likely to contribute to the replication of pRiA4b, were identified in the same orientation along the sequence.

L6 ANSWER 23 OF 26 MEDLINE DUPLICATE 16
AN 88194626 MEDLINE
DN 88194626
TI Evidence for **autonomous** replication and stabilization of recombinant plasmids in the transformants of yeast Hansenula polymorpha.
AU Tikhomirova L P; Ikonomova R N; Kuznetsova E N
CS Institute of Biochemistry and Physiology of Microorganisms, USSR Academy of Sciences, Pushchino, Moscow region..
SO CURRENT GENETICS, (1986) 10 (10) 741-7.
Journal code: CUG. ISSN: 0172-8083.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198808
AB For the transformation of the yeast Hansenula polymorpha we have constructed a set of hybrid plasmids carrying the LEU2 gene of Saccharomyces cerevisiae as a selective marker and fragments of mitochondrial DNA of Candida utilis and H. polymorpha or chromosomal DNA fragments of H. polymorpha as replicator sequences. The replication properties of chimeric plasmids in the yeast H. polymorpha were investigated. We showed that for plasmids propagated **autonomously** in this yeast the plasmid monomers could be detected in the transformants only during the immediate time after the transformation event. Further growth under selective conditions led to the selection of polymeric forms of plasmid DNA as it was clearly shown for transformants carrying **cosmid** pL2 with mtDNA fragment of C. utilis. Such transformants carrying polymerized plasmids showed a remarkably increased stability of the transformed phenotype. **Cosmid** pL2 was able to shuttle between Escherichia coli, S. cerevisiae and H. polymorpha, whereas plasmids with DNA fragments from H. polymorpha did not transform S. cerevisiae effectively.

L6 ANSWER 24 OF 26 MEDLINE
AN 85054601 MEDLINE
DN 85054601
TI Shuttle cloning vectors for the marine bacterium Vibrio parahaemolyticus.
AU Datta A R; Kaper J B; MacQuillan A M
SO JOURNAL OF BACTERIOLOGY, (1984 Nov) 160 (2) 808-11.
Journal code: HH3. ISSN: 0021-9193.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198503
AB Two **cosmid** cloning vectors containing lambda cos sequences and a 42-base-pair multipurpose cloning sequence were constructed.

pAD22 also contains a 1.4-kilobase TRP-**ARS** fragment from Saccharomyces cerevisiae. These **cosmids** transformed Escherichia coli and S. cerevisiae cells and could be mobilized into Vibrio parahaemolyticus strains with a conjugative plasmid, pRK2013. The **cosmid** pAD22 was genetically and structurally stable during passage through V. parahaemolyticus and E. coli strains.

L6 ANSWER 25 OF 26 MEDLINE DUPLICATE 17
AN 84245170 MEDLINE
DN 84245170
TI Molecular cloning of the yeast fatty acid synthetase genes, FAS1 and FAS2: illustrating the structure of the FAS1 cluster gene by transcript mapping and transformation studies.
AU Schweizer M; Lebert C; Holtke J; Roberts L M; Schweizer E
SO MOLECULAR AND GENERAL GENETICS, (1984) 194 (3) 457-65.
Journal code: NGP. ISSN: 0026-8925.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198410
AB From a Saccharomyces cerevisiae gene bank contained in the novel yeast **cosmid** shuttle vector pMS201 the fatty acid synthetase (FAS) genes FAS1 and FAS2 were isolated. FAS clones were identified by in situ colony hybridization using two yeast DNA probes apparently capable of producing avian FAS cross-reacting material (J. Carbon, personal communication). Classification as FAS1 or FAS2 clones was achieved by their specific transformation of fas1 and fas2 yeast mutants. By transcription mapping FAS1 was assigned to about 5.3 kb within 14.8 kb of chromosomal DNA covered by two genomically adjacent BamHI fragments. The FAS2 gene was localized on a single BamHI fragment of 25 kb. One of the FAS clones (FAS2) produces immunologically cross-reacting material in Escherichia coli. High frequency transformation of fas1 mutants was only observed with one subclone, pMS3021 , containing the intact FAS1 locus. Other DNA segments cloned in the same self-replicating vector but representing only part of FAS1 exhibited drastically lower transformation rates. As evident from this and from FAS1 /TRP1-cotransformation rates only the intact FAS1 gene in pMS3021 is capable of fas1 -mutant complementation. With partial FAS1 genes, even when coding for an intact equivalent of the mutated domain, their chromosomal integration is necessary for the expression of FAS. In integrative transformants the coexistence of integrated and **autonomously** replicating plasmid DNA was demonstrated. Both, the extrachromosomal and chromosomally integrated FAS DNA was mitotically unstable. Transformation studies using subcloned FAS1 DNA segments revealed the relative locations of the enoyl reductase and dehydratase domains within this pentafunctional cluster gene.

L6 ANSWER 26 OF 26 BIOSIS COPYRIGHT 1998 BIOSIS
AN 83:299465 BIOSIS
DN BA76:56957
TI MITOCHONDRIAL DNA SEQUENCES OF CANDIDA-UTILIS CAPABLE OF SUPPORTING **AUTONOMOUS** REPLICATION OF PLASMIDS IN SACCHAROMYCES-CEREVISIAE.
AU TIKHOMIROVA L P; KRYUKOV V M; STRIZHOV N I; BAYEV A A
CS INST. BIOCHEM. PHYSIOL. MICROORG., USSR ACAD. SCI., PUSHCHINO, MOSCOW REGION, 142292, USSR.
SO MOL GEN GENET 189 (3). 1983. 479-484. CODEN: MGGEAE ISSN: 0026-8925
LA English

AB DNA sequences of C. utilis capable of supporting **autonomous** replication of plasmids in S. cerevisiae were isolated by cloning HindIII restriction fragments of total DNA of C. utilis in the **cosmid** pHC79-arg4-43 carrying the gene of argininosuccinate-lyase as the selective marker for yeast transformation. Three hybrid plasmids replicating in S. cerevisiae were obtained and growth characteristics of plasmid-carrying cells were investigated. The hybridization experiments show that all hybrid plasmids obtained contain inserts of C. utilis DNA, all of mitochondrial origin. There was no hybridization to S. cerevisiae total DNA observed. One of the hybrid plasmids (pESC17) was characterized in detail. Localization of the replication origin of the cloned fragment was accomplished by recloning of subfragments in the plasmid pHC79-arg4-43. Effective replication in the yeast cells necessitates the presence of a 300 bp [base pair] sequence. A primary structure of this DNA fragment showed an extremely high AT content and the absence of GC blocks.

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	11.75	11.90

STN INTERNATIONAL LOGOFF AT 11:11:08 ON 13 APR 1998

Trying 9351006...Open

Welcome to STN International! Enter x:x
LOGINID:ssspta1805jxb
PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS	1	Feb 2	Web Page URLs for STN Seminar Schedule - N. America
NEWS	2	Mar 24	STN Express 4.1 with Discover! for Windows Now Available
NEWS	3	Mar 31	Free Connect Hour in KKF in April 1998
NEWS	4	Apr 10	Derwent World Patents Index (DWPI) Coverage Expanded to Include Mexico

NEWS EXPRESS	Discover! is Year 2000 Compliant
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* * * * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:22:56 ON 13 APR 1998

=> file medline, biosis

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.15	0.15

FILE 'MEDLINE' ENTERED AT 11:23:06 ON 13 APR 1998

FILE 'BIOSIS' ENTERED AT 11:23:06 ON 13 APR 1998
COPYRIGHT (C) 1998 BIOSIS(R)

=> s cosmid and (yeast or (schizosaccharomyces pombe))

L1 918 COSMID AND (YEAST OR (SCHIZOSACCHAROMYCES POMBE))

=> s l1 and (ars or autonomous?)

L2 11 L1 AND (ARS OR AUTONOMOUS?)

=> duplicate remove l2

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L2
L3 7 DUPLICATE REMOVE L2 (4 DUPLICATES REMOVED)

=> d 1-7 bib ab

L3 ANSWER 1 OF 7 MEDLINE DUPLICATE 1
AN 97245294 MEDLINE
DN 97245294
TI Sequence analysis of a 37.6 kbp **cosmid** clone from the right arm of Saccharomyces cerevisiae chromosome XII, carrying YAP3, HOG1, SNR6, tRNA-Arg3 and 23 new open reading frames, among which several homologies to proteins involved in cell division control and to mammalian growth factors and other animal proteins are found.
AU Verhasselt P; Volckaert G
CS Katholieke Universiteit Leuven, Laboratory of Gene Technology, Belgium.
SO YEAST, (1997 Mar 15) 13 (3) 241-50.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
OS GENBANK-A32646; GENBANK-B32646; GENBANK-D10017; GENBANK-L06279; GENBANK-S20150; GENBANK-T37940; GENBANK-U00043; GENBANK-X85802; GENBANK-X89154; GENBANK-Z47047; GENBANK-Z48179
EM 199708
AB The nucleotide sequence of 37,639 bp of the right arm of chromosome XII has been determined. Twenty-five open reading frames (ORFs) longer than 300 bp were detected, two of which extend into the flanking **cosmids**. Only two (L2931 and L2961) of the 25 ORFs correspond to previously sequenced genes (HOG1 and YAP3, respectively). Another ORF is distinct from YAP3 but shows pronounced similarity to it. About half of the remaining ORFs show similarity to other genes or display characteristic protein signatures. In particular, ORF L2952 has striking homology with the probable cell cycle control protein crn of Drosophila melanogaster. L2949 has significant similarity to the human ZFM1 (related to a potential suppressor oncogene) and mouse CW17R genes, though it lacks the carboxy-terminal oligoproline and oligoglutamine stretches encoded by these mammalian genes. The small ORF L2922 is similar to part of the much larger **yeast** flocculation gene FLO1. Other sequences found in the 37639 bp fragment are one delta and one solo-sigma element, the tRNA-Arg3 gene, the small nuclear RNA gene SNR6 and three **ARS** consensus sequences.

L3 ANSWER 2 OF 7 MEDLINE DUPLICATE 2
AN 97197984 MEDLINE
DN 97197984
TI The sequence of 32b on the left arm of **yeast** chromosome XII reveals six known genes, a new member of the seripauperins family and a new ABS transporter homologous to the human multidrug resistance protein.
AU Purnelle B; Goffeau A
CS Unite de Biochimie Physiologique, Universite Catholique de Louvain, Louvain-la-Neuve, Belgium.
SO YEAST, (1997 Feb) 13 (2) 183-8.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X97560
EM 199707
EW 19970703
AB The analysis of a 32 kb DNA fragment from **cosmid** 2G12 on the left arm of chromosome XII identifies 14 open reading frames (ORFs) numbered L0948 to L1325, a new tRNA for proline, a delta remnant and two putative **ARS**. Six ORFs have been previously identified: HSP104, SSA2, SPA2, KNS1, DPS1/APS and SDC25. Three putative ORFs have significant homology with known proteins: L0968 is a new member of the very large 'seripauperins' family, comprising at least 20 **yeast** members; L1313 is a new ABC transporter highly homologous to the **yeast** cadmium resistance protein Ycf1p and to the human multidrug resistance protein hMRP1; the C-terminal part of L1325 present in our sequence is very homologous to the fruit fly abdominal segment formation protein Pumilio. Finally, two ORFs, L1201 and L1205, have weak homology with two **yeast** hypothetical proteins of unknown function identified by the **yeast** systematic sequencing genome. Since our nucleotide sequence overlaps by 11.6 kb the **cosmid** 2B18 sequenced by Miosga and Zimmerman (1996) on the

right end, we have not reported here the analysis of the ORFs L1313, L1321 and L1325.

L3 ANSWER 3 OF 7 MEDLINE
AN 96021609 MEDLINE
DN 96021609
TI A 29.425 kb segment on the left arm of **yeast** chromosome XV contains more than twice as many unknown as known open reading frames.
AU Zumstein E; Pearson B M; Kalogeropoulos A; Schweizer M
CS Institute of Food Research, Genetics & Microbiology Department, Norwich Research Park, Colney, U.K.
SO YEAST, (1995 Aug) 11 (10) 975-86.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X83121; GENBANK-M73270
EM 199604
AB The nucleotide sequence of a 29.425 kb fragment localized on the left arm of chromosome XV from Saccharomyces cerevisiae has been determined. The sequence contains 13 open reading frames (ORFs) of which four encode the known genes ADH1, COQ3, MSH2 and RCF4. Predictions are made concerning the functions of the unknown ORFs. Some of the ORFs contain sequences similar to expressed sequence tags (EST) found in the database made available by TIGR. In particular, the highly expressed ADH1 gene is represented in this database by no less than 20 EST sequences. Two **ARS** sequences and a putative functional GCN4 motif have also been detected. One ORF (O0953) containing nine putative transmembrane segments is similar to a hypothetical membrane protein of Arabidopsis thaliana. Characteristic features of the other ORFs include ATP/GTP binding sites, a fungal Zn(2)-Cys(6) binuclear centre, an endoplasmic reticulum targeting sequence, a beta-transducin repeat signature and in two instances, good similarity to the prokaryotic lipoprotein signal peptide motif.

L3 ANSWER 4 OF 7 MEDLINE
AN 95112788 MEDLINE
DN 95112788
TI Complete DNA sequence of **yeast** chromosome II.
AU Feldmann H; Aigle M; Aljinovic G; Andre B; Baclet M C; Barthe C; Baur A; Becam A M; Biteau N; Boles E; et al
CS Institut fur Physiologische Chemie, Physikalische Biochemie und Zellbiologie, Universitat Munchen, Germany..
SO EMBO JOURNAL, (1994 Dec 15) 13 (24) 5795-809.
Journal code: EMB. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-Z35762; GENBANK-Z35763; GENBANK-Z35764; GENBANK-Z35765; GENBANK-Z35766; GENBANK-Z35767; GENBANK-Z35768; GENBANK-Z35769; GENBANK-Z35770; GENBANK-Z35771; GENBANK-Z35773; GENBANK-Z35774; GENBANK-Z35775; GENBANK-Z35776; GENBANK-Z35777; GENBANK-Z35778; GENBANK-Z35779; GENBANK-Z35780; GENBANK-Z35781; GENBANK-Z35782; GENBANK-Z35783; GENBANK-Z35784; GENBANK-Z35785; GENBANK-Z35786; GENBANK-Z35787; GENBANK-Z35788; GENBANK-Z35789; GENBANK-Z35790; GENBANK-Z35791; GENBANK-Z35792

EM 199504
AB In the framework of the EU genome-sequencing programmes, the complete DNA sequence of the **yeast** Saccharomyces cerevisiae chromosome II (807 188 bp) has been determined. At present, this is the largest eukaryotic chromosome entirely sequenced. A total of 410 open reading frames (ORFs) were identified, covering 72% of the sequence. Similarity searches revealed that 124 ORFs (30%) correspond to genes of known function, 51 ORFs (12.5%) appear to be homologues of genes whose functions are known, 52 others (12.5%) have homologues the functions of which are not well defined and another 33 of the novel putative genes (8%) exhibit a degree of similarity which is insufficient to confidently assign function. Of the genes on chromosome II, 37-45% are thus of unpredicted function. Among the novel putative genes, we found several that are related to genes that perform differentiated functions in multicellular organisms of are involved in malignancy. In addition to a compact arrangement of potential protein coding sequences, the analysis of this chromosome confirmed general chromosome patterns but also revealed particular novel features of chromosomal organization. Alternating regional variations in average base composition correlate with variations in local gene density along chromosome II, as observed in chromosomes XI and III. We propose that functional **ARS** elements are preferably located in the AT-rich regions that have a spacing of approximately 110 kb. Similarly, the 13 tRNA genes and the three Ty elements of chromosome II are found in AT-rich regions. In chromosome II, the distribution of coding sequences between the two strands is biased, with a ratio of 1.3:1. An interesting aspect regarding the evolution of the eukaryotic genome is the finding that chromosome II has a high degree of internal genetic redundancy, amounting to 16% of the coding capacity.

L3 ANSWER 5 OF 7 MEDLINE DUPLICATE 3
AN 88194626 MEDLINE
DN 88194626
TI Evidence for **autonomous** replication and stabilization of recombinant plasmids in the transformants of **yeast** Hansenula polymorpha.
AU Tikhomirova L P; Ikonomova R N; Kuznetsova E N
CS Institute of Biochemistry and Physiology of Microorganisms, USSR Academy of Sciences, Pushchino, Moscow region..
SO CURRENT GENETICS, (1986) 10 (10) 741-7.
Journal code: CUG. ISSN: 0172-8083.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198808
AB For the transformation of the **yeast** Hansenula polymorpha we have constructed a set of hybrid plasmids carrying the LEU2 gene of Saccharomyces cerevisiae as a selective marker and fragments of mitochondrial DNA of Candida utilis and H. polymorpha or chromosomal DNA fragments of H. polymorpha as replicator sequences. The replication properties of chimeric plasmids in the **yeast** H. polymorpha were investigated. We showed that for plasmids propagated **autonomously** in this **yeast** the plasmid monomers could be detected in the transformants only during the immediate time after the transformation event. Further growth under selective conditions led to the selection of polymeric forms of plasmid DNA as it was clearly shown for transformants carrying

cosmid pL2 with mtDNA fragment of C. utilis. Such transformants carrying polymerized plasmids showed a remarkably increased stability of the transformed phenotype. **Cosmid** pL2 was able to shuttle between Escherichia coli, S. cerevisiae and H. polymorpha, whereas plasmids with DNA fragments from H. polymorpha did not transform S. cerevisiae effectively.

L3 ANSWER 6 OF 7 MEDLINE DUPLICATE 4
AN 84245170 MEDLINE
DN 84245170
TI Molecular cloning of the **yeast** fatty acid synthetase genes, FAS1 and FAS2: illustrating the structure of the FAS1 cluster gene by transcript mapping and transformation studies.
AU Schweizer M; Lebert C; Holtke J; Roberts L M; Schweizer E
SO MOLECULAR AND GENERAL GENETICS, (1984) 194 (3) 457-65. Journal code: NGP. ISSN: 0026-8925.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198410
AB From a Saccharomyces cerevisiae gene bank contained in the novel **yeast cosmid** shuttle vector pMS201 the fatty acid synthetase (FAS) genes FAS1 and FAS2 were isolated. FAS clones were identified by in situ colony hybridization using two **yeast** DNA probes apparently capable of producing avian FAS cross-reacting material (J. Carbon, personal communication). Classification as FAS1 or FAS2 clones was achieved by their specific transformation of fas1 and fas2 **yeast** mutants. By transcription mapping FAS1 was assigned to about 5.3 kb within 14.8 kb of chromosomal DNA covered by two genomically adjacent BamHI fragments. The FAS2 gene was localized on a single BamHI fragment of 25 kb. One of the FAS clones (FAS2) produces immunologically cross-reacting material in Escherichia coli. High frequency transformation of fas1 mutants was only observed with one subclone, pMS3021 , containing the intact FAS1 locus. Other DNA segments cloned in the same self-replicating vector but representing only part of FAS1 exhibited drastically lower transformation rates. As evident from this and from FAS1 /TRP1-cotransformation rates only the intact FAS1 gene in pMS3021 is capable of fas1 -mutant complementation. With partial FAS1 genes, even when coding for an intact equivalent of the mutated domain, their chromosomal integration is necessary for the expression of FAS. In integrative transformants the coexistence of integrated and **autonomously** replicating plasmid DNA was demonstrated. Both, the extrachromosomal and chromosomally integrated FAS DNA was mitotically unstable. Transformation studies using subcloned FAS1 DNA segments revealed the relative locations of the enoyl reductase and dehydratase domains within this pentafunctional cluster gene.

L3 ANSWER 7 OF 7 BIOSIS COPYRIGHT 1998 BIOSIS
AN 83:299465 BIOSIS
DN BA76:56957
TI MITOCHONDRIAL DNA SEQUENCES OF CANDIDA-UTILIS CAPABLE OF SUPPORTING **AUTONOMOUS** REPLICATION OF PLASMIDS IN SACCHAROMYCES-CEREVISIAE.
AU TIKHOMIROVA L P; KRYUKOV V M; STRIZHOV N I; BAYEV A A
CS INST. BIOCHEM. PHYSIOL. MICROORG., USSR ACAD. SCI., PUSHCHINO, MOSCOW REGION, 142292, USSR.
SO MOL GEN GENET 189 (3). 1983. 479-484. CODEN: MGGEAE ISSN: 0026-8925
LA English

AB DNA sequences of C. utilis capable of supporting **autonomous** replication of plasmids in S. cerevisiae were isolated by cloning HindIII restriction fragments of total DNA of C. utilis in the **cosmid** pHC79-arg4-43 carrying the gene of argininosuccinate-lyase as the selective marker for **yeast** transformation. Three hybrid plasmids replicating in S. cerevisiae were obtained and growth characteristics of plasmid-carrying cells were investigated. The hybridization experiments show that all hybrid plasmids obtained contain inserts of C. utilis DNA, all of mitochondrial origin. There was no hybridization to S. cerevisiae total DNA observed. One of the hybrid plasmids (pESC17) was characterized in detail. Localization of the replication origin of the cloned fragment was accomplished by recloning of subfragments in the plasmid pHC79-arg4-43. Effective replication in the **yeast** cells necessitates the presence of a 300 bp [base pair] sequence. A primary structure of this DNA fragment showed an extremely high AT content and the absence of GC blocks.

=> d his

(FILE 'HOME' ENTERED AT 11:22:56 ON 13 APR 1998)

FILE 'MEDLINE, BIOSIS' ENTERED AT 11:23:06 ON 13 APR 1998
L1 918 S COSMID AND (YEAST OR (SCHIZOSACCHAROMYCES POMBE))
L2 11 S L1 AND (ARS OR AUTONOMOUS?)
L3 7 DUPLICATE REMOVE L2 (4 DUPLICATES REMOVED)

=> s l1 and vector

L4 102 L1 AND VECTOR

=> duplicate remove l4

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L4
L5 70 DUPLICATE REMOVE L4 (32 DUPLICATES REMOVED)

=> d 1-10 bib ab

L5 ANSWER 1 OF 70 MEDLINE DUPLICATE 1
AN 97149592 MEDLINE
DN 97149592
TI New fimbrial adhesins of Serratia marcescens isolated from urinary tract infections: description and properties.
AU Leranoz S; Orus P; Berlanga M; Dalet F; Vinas M
CS Department of Microbiology, Institut Universitari de Salut Publica de Catalunya, University of Barcelona, Spain.
SO JOURNAL OF UROLOGY, (1997 Feb) 157 (2) 694-8.
Journal code: KC7. ISSN: 0022-5347.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals; Cancer Journals
EM 199704
EW 19970404
AB Fimbriation, hemagglutination and adherence properties were studied

in two strains of S. marcescens (ATCC 43820 and 43821) isolated from the urine of two hospitalized patients in two different hospitals. Studies were performed using electron microscopy (EM), fimbrial purification, recombinant DNA and hemagglutination techniques, hydrophobicity and tests of adherence to uroepithelial cells, catheters and glass. In EM, fimbriae of these two strains showed an inner channel and were 11 nm. thick and 0.76-1.08 microns long. Original strains and the clone GH42-pSF192 (recombinant DNA prepared using E. coli GH42 as recipient and the **cosmid** SuperCos 1 as a **vector**) versus negative control (E. coli GH42-SuperCos 1) showed mannose-resistant hemagglutination of tanned erythrocytes and **yeast**, high hydrophobicity (55.4 and 49.6% at 37C versus 22.8%) and high adherence to borosilicate glass (313,000 and 168,000 CFU/cm.2 versus 17,000 CFU/cm.2), catheters (4.7 x 10(6) and 1.0 x 10(6) CFU/cm.2 versus 3.9 x 10(4) CFU/cm.2) and uroepithelial cells (adherence indexes of 3.82 and 3.29 versus 1.25). The properties of the fimbriae studied were different from those previously described in the genus Serratia, and they were designated as MR/T.

L5 ANSWER 2 OF 70 MEDLINE
AN 97341112 MEDLINE
DN 97341112
TI High-resolution mapping by YAC fragmentation of a 2.5-Mb Xp22 region containing the human RS, KFSD and CLS disease genes.
AU Van de Vosse E; Van der Bent P; Heus J J; Van Ommen G J; Den Dunnen J T
CS MGC-Department of Human Genetics, Leiden University, Wassenaarseweg 72, 2333 AL Leiden, The Netherlands.
SO MAMMALIAN GENOME, (1997 Jul) 8 (7) 497-501.
Journal code: BES. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199710
EW 19971001
AB The disease loci for X-linked Retinoschisis (RS), Keratosis follicularis spinulosa decalvans (KFSD), and Coffin-Lowry syndrome (CLS) have been localized to the same, small region in Xp22 on the human X Chromosome (Chr). To generate a high-resolution map of the available contig in this area, we have used the YAC fragmentation **vectors** pBP108/ADE2 and pBP109/ADE2 and generated fragmented YACs from a 2.5-Mb YAC (y939H7) spanning the mentioned disease gene candidate regions. Forty-seven fragmented YACs were generated and analyzed, ranging in size from 170 kb to over 2400 kb. The resulting YAC fragmentation panel was used to construct a detailed restriction map of the region and has been used to bin clones and markers. As a deletion panel, it will present a valuable resource for further mapping.

L5 ANSWER 3 OF 70 MEDLINE
AN 97237051 MEDLINE
DN 97237051
TI Human histone gene organization: nonregular arrangement within a large cluster.
AU Albig W; Kioschis P; Poustka A; Meergans K; Doenecke D
CS Institut fur Biochemie und Molekulare Zellbiologie, Universitat Gottingen, Germany.
SO GENOMICS, (1997 Mar 1) 40 (2) 314-22.

Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-Z80776; GENBANK-Z80777; GENBANK-Z80778; GENBANK-Z80779; GENBANK-Z80780; GENBANK-Z80781; GENBANK-Z80782; GENBANK-Z80783; GENBANK-Z80784; GENBANK-Z80785; GENBANK-Z80786; GENBANK-Z80787; GENBANK-Z80788; GENBANK-X67080; GENBANK-Z46261; GENBANK-X60481; GENBANK-X67081; GENBANK-X60487
EM 199706
EW 19970604
AB We have previously located the genes of the five human main type H1 genes and the gene encoding the testicular subtype H1t to the region 21.1 to 22.2 on the short arm of chromosome 6. To investigate the organization of the histone genes in this region, we isolated two YACs from a human YAC library by PCR screening with primers specific for histone H1.1. This screen revealed two YAC clones, YAC Y23 (corresponding to ICRFy901D1223) contains an insert of about 480 kb, whereas the smaller YAC 4A (corresponding to ICRFy900C104) spans about 340 kb and is completely covered by YAC Y23. We have subcloned the YAC inserts in **cosmids**, determined the linear orientation of the **cosmids** by **cosmid** walking, and constructed a restriction map of the entire region by mapping the individual **cosmids** using partial digests and hybridization with labeled oligonucleotides complementary to the cos site of the **vector**. Hybridization analysis, subcloning, restriction mapping, and sequencing revealed that most of the previously isolated phage and **cosmid** clones containing histone genes are part of this YAC including the clones containing the four human main type H1 histone genes H1.1 to H1.4, the H1t gene, and core histone genes. Thirty-five histone genes map within 260 kb of the YAC Y23 insert. All newly identified histone genes were sequenced, and the sequences were deposited with the EMBL nucleotide sequence database. The histone H1.5 gene is not part of this region, and we therefore conclude that the H1.5 gene and the associated core histone genes form a separate subcluster within this chromosomal region.

L5 ANSWER 4 OF 70 MEDLINE
AN 97196605 MEDLINE
DN 97196605
TI Improved method for the construction of **cosmid** sublibraries from **yeast** artificial chromosomes.
AU Muller H W; Meese E U
CS University of the Saar Medical School, Homburg/Saar, Germany.
SO BIOTECHNIQUES, (1997 Feb) 22 (2) 264-6, 268.
Journal code: AN3. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199707
EW 19970702

L5 ANSWER 5 OF 70 MEDLINE DUPLICATE 2
AN 97245296 MEDLINE
DN 97245296
TI The DNA sequence of **cosmid** 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of

overlapping open reading frames.
AU De Antoni A; D'Angelo M; Dal Pero F; Sartorello F; Pandolfo D; Pallavicini A; Lanfranchi G; Valle G
CS Dipartimento di Biologia, Universit`a degli Studi di Padova, Italy.
SO YEAST, (1997 Mar 15) 13 (3) 261-6.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-Z69382
EM 199708
EW 19970802
AB This work is part of the effort for sequencing chromosome XIV of Saccharomyces cerevisiae. **Cosmid** 14-13b contains a 37.8 kb insert derived from a partial Sau3A digestion of the genome, cloned into the BamHI site of the **vector** Pou6. The strategy used for sequencing is based on the fragmentation of the whole **cosmid** by sonication, followed by shotgun sequencing on an Applied Biosystem DNA sequencer. The clones with inserts corresponding to the **vector** were identified by dot-blot hybridization, without the need of sequencing. The analysis of the DNA sequence reveals 29 open reading frames (ORFs) longer than 300 bases. Nine ORFs are internal to some other ORFs. Similarity searches against DNA and protein data banks show that six ORFs correspond to already known **yeast** genes (OMP1, PSU1, MLS1, RPC19, DBP2, CYB5) and one ORF matches the sequence of a putative **yeast** gene (ESBP6).

L5 ANSWER 6 OF 70 MEDLINE
AN 97155325 MEDLINE
DN 97155325
TI Identification of polygenic disease genes.
AU Cox R D
CS Wellcome Trust Centre for Human Genetics, Headington, Oxford, UK.
SO JOURNAL OF RHEUMATOLOGY, (1997 Jan) 24 (1) 202-5.
Journal code: JWX. ISSN: 0315-162X.
CY Canada
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199705
EW 19970505
AB I discuss the identification and cloning of genes involved in determining susceptibility to diseases under polygenic control. The process of cloning a susceptibility gene is as follows: identification of new genetic markers in the region by database analysis, isolation of DNA clones in the region and the generation of new genetic markers, refinement of the map position using these markers for linkage disequilibrium analysis, construction of a physical and disequilibrium map, construction of a clone contig across the critical region in **yeast** artificial chromosomes, PAC, bacterial artificial chromosomes and **cosmids**, and finally gene identification and etiological mutation detection.

L5 ANSWER 7 OF 70 MEDLINE DUPLICATE 3
AN 97312658 MEDLINE
DN 97312658
TI Identification of a ferritin light chain pseudogene near the

glycerol kinase locus in Xp21 by cDNA amplification for identification of genomic expressed sequences.
AU Guo W; Adams V; Mason J; McCabe E R
CS Department of Pediatrics, UCLA School of Medicine 90095-1752, USA.
NC RO1 HD22563 (NICHD)
P30 HD24064 (NICHD)
P30 HD27823 (NICHD)
+
SO BIOCHEMICAL AND MOLECULAR MEDICINE, (1997 Apr) 60 (2) 169-73.
Journal code: B3J. ISSN: 1077-3150.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199709
EW 19970902
AB We used cDNA amplification for identification of genomic expressed sequences (CAIGES) to identify genes in the glycerol kinase region of the human X chromosome. During these investigations we identified the sequence for a ferritin light chain (FTL) pseudogene in this portion of Xp21. A human liver cDNA library was amplified by **vector** primers, labeled, and hybridized to Southern blots of EcoRI-digested human genomic DNA from **cosmids** isolated from **yeast** artificial chromosomes in the glycerol kinase region of Xp21. A 3.1-kb restriction fragment hybridized with the cDNA library, was subcloned and sequenced, and a 440-bp intronless sequence was found with strong similarity to the FTL coding sequence. Therefore, the FTL pseudogene that had been mapped previously to Xp22.3-21.2 was localized specifically to the glycerol kinase region. The CAIGES method permits rapid screening of genomic material and will identify genomic sequences with similarities to genes expressed in the cDNA library used to probe the cloned genomic DNA, including pseudogenes.

L5 ANSWER 8 OF 70 MEDLINE
AN 97208018 MEDLINE
DN 97208018
TI Construction and use of **cosmid** contigs.
AU Fairweather N
CS Wellcome Trust Centre for Human Genetics, University of Oxford, UK.
SO METHODS IN MOLECULAR BIOLOGY, (1997) 68 137-48.
Journal code: BU3. ISSN: 1064-3745.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199708
EW 19970801

L5 ANSWER 9 OF 70 MEDLINE DUPLICATE 4
AN 96349105 MEDLINE
DN 96349105
TI Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a **yeast** artificial chromosome.
AU Sorokin A; Azevedo V; Zumstein E; Galleron N; Ehrlich S D; Serror P
CS Laboratoire de Genetique Microbienne, Institut National de la Recherche Agronomique, Jouy en Josas, France..
sorokine@biotec.jouy.inra.fr
SO MICROBIOLOGY, (1996 Aug) 142 (Pt 8) 2005-16.

Journal code: BXW. ISSN: 1350-0872.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L47648; GENBANK-L47709; GENBANK-L47838; GENBANK-L09228; GENBANK-M80926; GENBANK-M80245
EM 199612
AB The standard strategies of genome sequencing based on lambda-**vector** or **cosmid** libraries are only partially applicable to AT-rich Gram-positive bacteria because of the problem of instability of their chromosomal DNA in heterologous hosts like Escherichia coli. One complete collection of ordered clones known for such bacteria is that of Bacillus subtilis, established by using **yeast** artificial chromosomes (YACs). This paper reports the results of the direct use of one of the YAC clones from the above collection for the sequencing of the region cloned in it. The strategy applied consisted of the following: (i) construction of M13 banks of the partially purified YAC DNA and sequencing of 800 M13 clones chosen at random; (ii) directed selection of M13 clones to sequence by using marginal contig fragments as hybridization probes; (iii) direct sequencing of joining PCR fragments obtained by combinations of primers corresponding to the ends of representative contigs. The complete 104,109 bp insert sequence of this YAC clone was thus established. The strategy used allowed us to avoid resequencing the two largest, previously sequenced, contigs (13,695 and 20,303 bp) of the YAC insert. We propose that the strategy used can be applied to the sequencing of the whole bacterial genome without intermediate cloning, as well as for larger inserts of eukaryotic origin cloned in YACs. Sequencing of the insert of the YAC clone 15-6B allowed us to establish the contiguous sequence of 127 kb from spollA to kdg. The organization of the newly determined region is presented. Of the 138 ORFs identified in the spollA-kdg region, 57 have no clear putative function from their homology to proteins in the databases.

L5 ANSWER 10 OF 70 MEDLINE DUPLICATE 5
AN 96202339 MEDLINE
DN 96202339
TI Sequence scanning: A method for rapid sequence acquisition from large-fragment DNA clones.
AU Nurminsky D I; Hartl D L
CS Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA.
NC HG01250 (NHGRI)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Feb 20) 93 (4) 1694-8.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199609
AB A strategy of "sequence scanning" is proposed for rapid acquisition of sequence from clones such as bacteriophage P1 clones, **cosmids**, or **yeast** artificial chromosomes. The approach makes use of a special **vector**, called LambdaScan, that reliably yields subclones with inserts in the size range 8-12 kb. A number of subclones, typically 96 or 192, are chosen at random, and the ends of the inserts are sequenced using

vector-specific primers. Then long-range spectrum PCR is used to order and orient the clones. This combination of shotgun and directed sequencing results in a high-resolution physical map suitable for the identification of coding regions or for comparison of sequence organization among genomes. Computer simulations indicate that, for a target clone of 100 kb, the scanning of 192 subclones with sequencing reads as short as 350 bp results in an approximate ratio of 1:2:1 of regions of double-stranded sequence, single-stranded sequence, and gaps. Longer sequencing reads tip the ratio strongly toward increased double-stranded sequence.

=> d 11-20 bib ab

L5 ANSWER 11 OF 70 MEDLINE DUPLICATE 6
AN 96235271 MEDLINE
DN 96235271
TI Isolation of the human chromosome 22q telomere and its application to detection of cryptic chromosomal abnormalities.
AU Ning Y; Rosenberg M; Biesecker L G; Ledbetter D H
CS Diagnostic Development Branch, National Institutes of Health, Bethesda, MD 20892, USA.
SO HUMAN GENETICS, (1996 Jun) 97 (6) 765-9.
Journal code: GED. ISSN: 0340-6717.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199609
AB A number of human telomeres have been successfully cloned using a modified **yeast** artificial chromosome (YAC) **vector** (half-YAC) cloning strategy, but to date, human chromosome 22q has not been identified by this approach. We used an alternative approach of genomic walking, starting from a subtelomeric sequence, Tel-Bam3.4. present on a number of human chromosomes including 22q. This approach was successful in the development of a **cosmid** contig representing the terminal 140 kb of human chromosome 22q, providing telomeric closure of the genetic and physical maps for 22q. The most distal region of the contig contains subtelomeric repeats which crosshybridize to a number of chromosomes, while the proximal sequences are unique for 22q. The unique sequence **cosmid** was used as a 22qter-specific probe for fluorescence in situ hybridization (FISH) analysis, which confirmed that this **cosmid** was distal to the most telomeric marker previously available for chromosome 22. In addition, this **cosmid** was used to document a 22q terminal deletion that was not detectable by conventional cytogenetic analysis. Unique telomere-specific FISH probes such as this one will have significant diagnostic value in the detection of cryptic deletions and translocations in patients with unexplained mental retardation and other patient populations.

L5 ANSWER 12 OF 70 MEDLINE DUPLICATE 7
AN 97080522 MEDLINE
DN 97080522
TI Assembly and extension of **yeast** artificial chromosomes to build up a large locus.
AU Popov A V; Butzler C; Frippiat J P; Lefranc M P; Bruggemann M
CS Department of Development and Genetics, Babraham Institute, Cambridge, UK.. andrei.popov@bbsrc.ac.uk
SO GENE, (1996 Oct 24) 177 (1-2) 195-201.

Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199702
EW 19970204
AB For the assembly of a large human locus, overlapping regions on **yeast** artificial chromosomes (YACs) and **cosmids** were linked up using their regions of homology. By site-specific recombination a YAC of 410 kb was created accommodating the major part of the human lambda light chain locus in authentic configuration with 28 variable (V) genes, all joining (J) segments, all constant (C) genes and the downstream enhancer. A contiguous region was first constructed from three overlapping **cosmids** . Each of these was linearized at unique sites in the **vectors** and YAC arms were ligated to the 5' and 3' ends. After cells of Saccharomyces cerevisiae were transformed with the three **cosmids**, YACs of 120 kb were obtained which contained the reassembled 3' J-C region in authentic configuration. The assembled YAC was further extended by mitotic recombination with a YAC containing a 280-kb region of the C-proximal part of the V gene cluster with a 15-kb 3' overlap. For this, a simple three-way selection procedure was developed involving the integration of different selectable marker genes at specific sites in the left and right YAC arms. Rare recombination events between two overlapping YACs could be identified in **yeast** clones able to grow in lysine- and adenine-deficient medium in the presence of 5-fluoro-orotic acid which is toxic for **yeast** cells containing a YAC with a functional URA3 gene. This approach made it possible to assemble and extend large YACs from an unlimited number of smaller overlapping YACs by positive-negative selection.

L5 ANSWER 13 OF 70 MEDLINE
AN 96167713 MEDLINE
DN 96167713
TI Covering YAC-cloned DNA with phages and **cosmids**.
AU Ragoussis J; Monaco A P
CS Paediatric Research Unit, United Medical School of Guy's Hospital, London, UK.
SO METHODS IN MOLECULAR BIOLOGY, (1996) 54 157-66.
Journal code: BU3. ISSN: 1064-3745.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199606

L5 ANSWER 14 OF 70 MEDLINE
AN 96129600 MEDLINE
DN 96129600
TI Isolation and characterization of a 1 Mb region of 5q23.3-q31.2 surrounding the human lysyl oxidase gene.
AU McAlinden T P; Smith D I; Smith S E; Krawetz S A
CS Department of Obstetrics and Gynecology, Wayne State University School of Medicine, Detroit, MI 48201, USA.
SO JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1995 Oct) 27 (10) 2409-13.
Journal code: J72. ISSN: 0022-2828.
CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB Lysyl oxidase (EC 1.4.3.13) plays a pivotal role in the maintenance of tissue integrity in both the normal and pathological states. It is a member of a newly discovered gene family that exhibits a complex mode of regulation. To date the resources necessary to begin to address its regulation have not been assembled. In part, this reflects the instability of this region of the genome when cloned into **cosmid vectors**. The paucity of long range restriction endonuclease sites suitable for mapping this region of the genome has further hampered progress. To begin to address this issue 2 YAC clones of 920 kb and 245 kb that contain the human lysyl oxidase gene were isolated. Long range physical mapping revealed that the 245 kb clone was centrally located within the 920 kb clone. The corresponding map of this region is congruent with that observed in the human genome. Thus, these YACs faithfully represent this region of the human genome. The results of our cloning and mapping studies described in this communication should accelerate the advance of our understanding of this new connective tissue gene family.

L5 ANSWER 15 OF 70 MEDLINE DUPLICATE 8
AN 96121380 MEDLINE
DN 96121380
TI A new human gene located in the PKD1 region of chromosome 16 is a functional homologue to ERV1 of **yeast**.
AU Lisowsky T; Weinstat-Saslow D L; Barton N; Reeders S T; Schneider M C
CS Botanisches Institut I, Universitat Dusseldorf, Germany.
NC 1-K11-DK02216-01 (NIDDK)
DK 40703 (NIDDK)
SO GENOMICS, (1995 Oct 10) 29 (3) 690-7.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U31176
EM 199605
AB A new human gene has been identified on chromosome 16 in the interval containing the locus for polycystic kidney disease (PKD1) by analysis of a genomic **cosmid** clone and cDNAs. The gene contains at least one intron and is actively transcribed in tissues from kidney and brain. The putative gene product is predicted to be homologous to the **yeast** scERV1 protein by virtue of the high degree of identity (42%) over the entire length of the polypeptides. In former studies the **yeast** scERV1 gene was found to be essential for oxidative phosphorylation, the maintenance of mitochondrial genomes, and the cell-division cycle. In this study a **yeast** expression **vector** with a chimeric reading frame coding for the first 21 amino acids of the **yeast** protein and the terminal 100 amino acid residues of the human factor was transformed into **yeast** mutants with two different defects for scERV1. The chimeric human gene product was able to complement the **yeast** mutants and restored near normal viability. This identifies the human gene as a structural and functional homologue of the scERV1 gene.

L5 ANSWER 16 OF 70 MEDLINE
AN 95206949 MEDLINE
DN 95206949
TI The construction and analysis of M13 libraries prepared from YAC DNA.
AU Vaudin M; Roopra A; Hillier L; Brinkman R; Sulston J; Wilson R K; Waterston R H
CS Department of Genetics, Washington University School of Medicine, St. Louis, MO 63108.
NC HG00956 (NHGRI)
SO NUCLEIC ACIDS RESEARCH, (1995 Feb 25) 23 (4) 670-4.
Journal code: O8L. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199506
AB **Yeast** artificial chromosomes (YACs) provide a powerful way to isolate and map large regions of genomic DNA and their use in genome analysis is now extensive. We modified a series of procedures to produce high quality shotgun libraries from small amounts of YAC DNA. Clones from several different libraries have been sequenced and analyzed for distribution, sequence integrity and degree of contamination from **yeast** DNA. We describe these procedures and analyses and show that sequencing at about 1-fold coverage, followed by database comparison (survey sequencing) offers a relatively quick method to determine the nature of previously uncharacterized **cosmid** or YAC clones.

L5 ANSWER 17 OF 70 MEDLINE
AN 96096515 MEDLINE
DN 96096515
TI Construction of a cDNA library for a specific region of a chromosome using a novel cDNA selection method utilizing latex particles.
AU Hayashida N; Sumi Y; Wada T; Handa H; Shinozaki K
CS Laboratory of Plant Molecular Biology, Institute of Physical and Chemical Research (RIKEN), Tsukuba, Japan.
SO GENE, (1995 Nov 20) 165 (2) 155-61.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-Z17671; GENBANK-Z17441; GENBANK-Z33712; GENBANK-Z34855; GENBANK-M20308; GENBANK-Z29012; GENBANK-Z29013; GENBANK-Z26111; GENBANK-D15786; GENBANK-D23969; GENBANK-D24404; GENBANK-X63701; GENBANK-T20994; GENBANK-Z28479; GENBANK-T14529; GENBANK-M23984; GENBANK-U05572; GENBANK-M82822; GENBANK-T14069; GENBANK-T13822; GENBANK-D16457; GENBANK-T04151; GENBANK-T13030
EM 199603
AB A novel method is described for the rapid concentration of particular cDNAs and their mapping to specific regions of a genome. The strategy for 'cDNA scanning' is based on the hybridization of an entire library of cDNAs to a large fragment of genomic DNA that is covalently bound to latex particles. The hybridized cDNAs are eluted, amplified by PCR and cloned into a lambda **vector**. Selected cDNAs that hybridized to the genomic DNA are cloned, with subsequent sequence analysis. Region-specific DNA fragments prepared from a **yeast** artificial chromosome (YAC) clone, EG10D9, which maps to chromosome 5 of the small cruciferous plant

Arabidopsis thaliana (At), were used to prepare a model system and were covalently bound to latex particles. cDNAs that hybridized to EG10D9 were concentrated by hybridization to the immobilized DNA. The hybridized cDNAs were recovered and amplified by PCR. The resultant sub-library of cDNAs of 0.5-2 kb in length was enriched about 1000-fold. The partial sequences of the cDNAs provided information about genes that are located on the EG10D9 region of the At genome. The cDNA scanning strategy provides an efficient method for the mapping of expressed genes which could be used as expressed sequence tags (EST) within a genome.

L5 ANSWER 18 OF 70 MEDLINE DUPLICATE 9
AN 95250370 MEDLINE
DN 95250370
TI Construction of a complete genomic library of Saccharomyces cerevisiae and physical mapping of chromosome XI at 3.7 kb resolution.
AU Thierry A; Gaillon L; Galibert F; Dujon B
CS Department de Biologie Moleculaire (URA 1149 du CNRS and UFR927 Universite P.M. Curie), Institut Pasteur, Paris, France..
SO YEAST, (1995 Feb) 11 (2) 121-35.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199508
AB A consortium of European laboratories has been organized to systematically sequence the genome of Saccharomyces cerevisiae. As part of the BIOTECH program aimed at sequencing chromosomes XI and II, we have constructed a total genomic library of **yeast** strain FY1679 (a direct S288C derivative) into **cosmid vectors** pWE15 and pOU61cos. Primary clones from four independent libraries totalling 190 genome equivalents have been stored at -80 degrees C. A subset of 1939 independent clones (six genome equivalents) was hybridized using purified chromosomes XI and X as probes. A total of 147 chromosome XI-specific **cosmid** clones was used to construct the physical map of that chromosome. Mapping methods included a combination of classical bottom-up strategies (fingerprinting, hybridizations) and a novel top-down strategy using I-SceI chromosome fragmentation. The 147 **cosmid** clones form a unique contig covering the entire chromosome XI (666 kb) with the sole exceptions of the (C1-3A)n repeats of the telomeres. Colinearity of **cosmid** inserts with **yeast** DNA was directly verified. A complete EcoRI map of chromosome XI was deduced from partial overlaps of **cosmids** and used for the sequencing program. Comparison of this map with the genetic map shows unexpected divergences that have been solved by subsequent genetic analysis, yet underline the necessity of independent physical mapping in genome projects.

L5 ANSWER 19 OF 70 MEDLINE
AN 96159518 MEDLINE
DN 96159518
TI Construction and utility of a human chromosome 22-specific Fosmid library.
AU Kim U J; Shizuya H; Sainz J; Garnes J; Pulst S M; de Jong P; Simon M I
CS Division of Biology, California Institute of Technology, Pasadena 91125, USA.

SO GENETIC ANALYSIS, (1995 Oct) 12 (2) 81-4.
Journal code: CEK.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB We have previously demonstrated the capability of the Fosmid **vector** based on Escherichia coli F-factor replicon to stably propagate **cosmid**-sized human genomic DNA fragments. Using the Fosmid **vector**, we have constructed and arrayed a 10 x human chromosome 22-specific library, partly by picking human positive clones from a total Fosmid library constructed using DNA from human-hamster hybrid cell line containing human chromosome 22, and partly by using flow-sorted chromosomal DNA. The clones and physical contig maps of the clones in the library will serve as a valuable resource for detailed analysis of the chromosome by providing reliable materials for high resolution mapping and sequencing. In order to efficiently build physical maps for the chromosomal regions of interest spanning several hundred kilobases to a megabase, it is necessary to rapidly identify subsets of the Fosmid clones from the library that cover such regions. In this report, we describe a method of using random amplification products derived from YAC clones to rapidly identify a subset of Fosmid clones that cover a specific genomic subregion.

L5 ANSWER 20 OF 70 MEDLINE DUPLICATE 10
AN 94173713 MEDLINE
DN 94173713
TI Rapid sequential walking from termini of **cosmid**, P1 and YAC inserts.
AU Wesley C S; Myers M P; Young M W
CS Howard Hughes Medical Institute, Rockefeller University, New York, NY 10021..
SO NUCLEIC ACIDS RESEARCH, (1994 Feb 11) 22 (3) 538-9.
Journal code: O8L. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199406

=> d 21-30 bib ab

L5 ANSWER 21 OF 70 MEDLINE
AN 95003633 MEDLINE
DN 95003633
TI Towards cloning the familial breast-ovarian cancer gene on chromosome 17.
AU Brown M A; Solomon E
CS Somatic Cell Genetics Laboratory, Imperial Cancer Research Fund, London, UK..
SO CURRENT OPINION IN GENETICS AND DEVELOPMENT, (1994 Jun) 4 (3) 439-45. Ref: 74
Journal code: BJC. ISSN: 0959-437X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)

LA English
FS Priority Journals
EM 199501
AB The past year has seen a great deal of excitement in the field of breast cancer genetics. Since linkage of the familial breast-ovarian cancer gene (BRCA1) to chromosome 17, the critical region has been narrowed to 1.0-1.5 Mb by recombination studies, a detailed physical map has been constructed and much of the region has been cloned in **yeast** artificial chromosome, bacteriophage P1 and **cosmid vectors**. The focus now lies on identifying the genes housed within the BRCA1 region and scanning them for oncogenic mutations.

L5 ANSWER 22 OF 70 MEDLINE DUPLICATE 11
AN 95163395 MEDLINE
DN 95163395
TI Organization of heterologous DNA inserts on the mouse meiotic chromosome core.
AU Heng H H; Tsui L C; Moens P B
CS Department of Molecular and Medical Genetics, University of Toronto, Ontario, Canada..
SO CHROMOSOMA, (1994 Oct) 103 (6) 401-7.
Journal code: D7A. ISSN: 0009-5915.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199505
AB With simultaneous immunofluorescence and fluorescent in situ hybridization, we have determined the organization of native and heterologous DNA sequences relative to the cores of meiotic prophase chromosomes. The normal chromatin organization is demonstrated with probes of mouse sequences: a **cosmid** probe that identifies unique sequences and a 720 kb **yeast** artificial chromosome (YAC) probe that recognizes a specific region of the chromatin domain. The heterologous DNA consists of a 1.8 Mb insertion of 40 tandem head-to-tail phage lambda LIZ **vectors** and of 11.4 Mb of bacterial/mouse DNA repeats. The lengthy lambda insert is unusual in that it is not contained in the chromatin domain of chromosome 4 and in that it fails to form direct attachments to the chromosome core. The ends are attached indirectly, probably by means of the flanking mouse sequences. At late stages of meiotic prophase, while the terminal attachments remain the same, the lambda DNA becomes highly compacted. Apparently, higher order condensation and core attachment are independent processes. The condensed inserts relax precociously at metaphase I. In the mouse heterozygous for the insert, the two sister inserts are usually merged, as are all four inserts in the homozygous mouse. Evidently chromatin loops with identical sequences can become associated during meiotic prophase. Mouse sequences within a heterologous DNA insert (repeats of bacterial plasmid pBR322 with a mouse beta-globin insert) were observed to restore some degree of core attachment.

L5 ANSWER 23 OF 70 MEDLINE
AN 94319085 MEDLINE
DN 94319085
TI Efficient identification and regional positioning of YAC and **cosmid** clones to human chromosome 21 by radiation fusion hybrids.
AU Kumlien J; Labella T; Zehetner G; Vatcheva R; Nizetic D; Lehrach H

CS Department of Genome Analysis, Imperial Cancer Research Fund, London, UK..
SO MAMMALIAN GENOME, (1994 Jun) 5 (6) 365-71.
Journal code: BES. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199411
AB The use of integrated mapping strategies involving bacterial, **yeast**, and rodent cells as hosts simplifies the construction of maps, which combine long-range order, high resolution, and easy access to the cloned DNA. Radiation-fusion hybrids offer a specially powerful long-range mapping system for human chromosomes. We describe here techniques for establishing a radiation-fusion hybrid map of Chromosome (Chr) 21q and its integration with local information on YAC and **cosmid** positions.

L5 ANSWER 24 OF 70 MEDLINE
AN 95102109 MEDLINE
DN 95102109
TI Construction of a **cosmid** contig and of an EcoRI restriction map of **yeast** chromosome X.
AU Huang M E; Chuat J C; Thierry A; Dujon B; Galibert F
CS Laboratoire de Biochimie et Biologie Moleculaire, Unite de Recombinaisons Genetiques (UPR 41-CNRS), Faculte de Medecine, Rennes, France..
SO DNA SEQUENCE, (1994) 4 (5) 293-300.
Journal code: A9H. ISSN: 1042-5179.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199504
AB We report here the construction of a complete physical map of the chromosome X of **yeast** Saccharomyces cerevisiae. Fragments resulting from partial Sau3AI digestion of DNA from a diploid strain derived from S288C were ligated to linearized pWE15, a **cosmid vector** with T3 and T7 promoters. Another library, made in the **cosmid vector** pOU61 cos, that lacks T3 and T7 promoters, was also used as a source of target clones. Chromosome-X-specific clones were sorted out by hybridization with radiolabelled pulse-field-gel-purified chromosome X as a probe. Then, 254 **cosmids** were ordered by walking from one to another by hybridization with end-specific T3 or T7 RNA transcripts as probes. The construction was put to the test by hybridization with a battery of chromosome X gene markers, that showed that the physical map and the genetic map were colinear. The validity of the contig was further strengthened by the results of chromosome nested fractionation with meganuclease I-SceI. An EcoRI restriction map of the contig enabled further verification and measurement of the total length of the contig, that was found to be approximately 700 kb in size. In addition to providing a base for the ongoing **yeast** genome sequencing project, the physical map can be used to map any sequence belonging to chromosome X.

L5 ANSWER 25 OF 70 MEDLINE DUPLICATE 12
AN 95162952 MEDLINE
DN 95162952
TI **Yeast** artificial chromosome cloning.

AU Ramsay M
CS Department of Human Genetics, School of Pathology, South African Institute for Medical Research, Johannesburg..
SO MOLECULAR BIOTECHNOLOGY, (1994 Apr) 1 (2) 181-201. Ref: 74
Journal code: B97. ISSN: 1073-6085.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199505
AB **Yeast** artificial chromosome (YAC) cloning systems enable the cloning of DNA stretches of 50 to well over 2000 kb. This makes it possible to study large intact regions of DNA in detail, by restriction mapping the YAC to produce a physical map and by examining the YAC for coding sequences or genes. YACs are important for their ability to clone the complete sequences of large genes or gene complexes that exceed the size limit for cloning in conventional bacterial cloning **vectors** like plasmids (up to 10 kb), bacteriophage (15 kb), and **cosmids** (50 kb). A major advantage of cloning in **yeast**, a eukaryote, is that many sequences that are unstable, underrepresented, or absent when cloned into prokaryotic systems, remain stable and intact in YAC clones. It is possible to reintroduce YACs intact into mammalian cells where the introduced mammalian genes are expressed and used to study the functions of genes in the context of flanking sequences. The correct protein processing mechanisms are present in the mammalian cells to ensure that a viable protein product is produced.

L5 ANSWER 26 OF 70 MEDLINE
AN 95226125 MEDLINE
DN 95226125
TI Construction and preliminary analysis of the ICRF human P1 library.
AU Francis F; Zehetner G; Hoglund M; Lehrach H
CS Genome Analysis Laboratory, Imperial Cancer Research Fund (ICRF), London, England..
SO GENETIC ANALYSIS, TECHNIQUES AND APPLICATIONS, (1994) 11 (5-6) 148-57.
Journal code: AP4. ISSN: 1050-3862.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199507
AB P1 clone libraries have now been established as effective complements to **cosmid** and **yeast** artificial chromosome libraries in long-range mapping projects. To allow general access to P1 clones, we have constructed human and mouse P1 libraries. Clones have been picked into microtiter plates and used to prepare high-density filter grids, providing an efficient and easy screening system. Filters are being made available to other laboratories through the Reference Library System. In this work, we have developed a reliable protocol for generating P1 clones, based on the use of pulsed-field gel electrophoresis for size selection of DNA. A 1.2x genome coverage human library has been produced using this method. A preliminary analysis of this library is described.

L5 ANSWER 27 OF 70 MEDLINE DUPLICATE 13
AN 95138626 MEDLINE

DN 95138626
TI Physical and genetic mapping at the ATA/ATC locus on chromosome 11q22-23.
AU Rotman G; Savitski K; Vanagaite L; Bar-Shira A; Ziv Y; Gilad S; Uchenik V; Smith S; Shiloh Y
CS Department of Human Genetics, Sackler School of Medicine, Tel Aviv University, Israel..
SO INTERNATIONAL JOURNAL OF RADIATION BIOLOGY, (1994 Dec) 66 (6 Suppl) S63-6.
Journal code: IRB. ISSN: 0955-3002.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199505
AB Genetic heterogeneity in ataxia-telangiectasia (A-T) points to four different genes responsible for this disease. The two major A-T genes, ATA and ATC, were localized by genetic analysis close to each other on chromosome 11q22-23, prompting efforts of positional cloning. Essential steps in positional cloning are long-range cloning of the genomic region of interest, and derivation of highly polymorphic markers that would allow further reduction of the interval carrying the A-T gene. We constructed genomic contigs across the D11S611-D1S424 region harbouring the ATA and ATC genes in **yeast** artificial chromosome (YAC) **vectors**. These contigs were used as a fine mapping tool and enabled us to localize along the A-T region, eight microsatellite markers generated randomly by genome mapping centres. In addition, we used specific YAC clones to generate five new microsatellite markers based on polymorphic CA repeats. Recombination mapping based on Israeli A-T families indicates that the ATC gene is distal to the locus D11S1817. Further linkage analysis using these markers is expected to reduce the major A-T locus considerably to a size appropriate for **cosmid** cloning and identification of transcribed sequences.

L5 ANSWER 28 OF 70 BIOSIS COPYRIGHT 1998 BIOSIS
AN 94:391011 BIOSIS
DN 97404011
TI Rapid isolation of **cosmid** insert DNA by triple-helix-mediated affinity capture.
AU Ji H; Smith L M; Guilfoyle R A
CS Dep. Chem., Univ. Wisconsin-Madison, Madison, WI 53706, USA
SO Genetic Analysis Techniques and Applications 11 (2). 1994. 43-47.
ISSN: 1050-3862
LA English
AB A simple and rapid method for the isolation of **cosmid** insert DNA was developed based on triple-helix-mediated affinity capture (TAC). A modified **cosmid** was constructed from the SuperCos 1 **cosmid vector** by flanking the cloning site with two homopurine-homopyrimidine triple-helix-forming sequences. The **cosmid** DNA is digested with NotI restriction enzyme to release the insert DNA. The NotI-digested **cosmid** DNA is then combined with a biotinylated homopyrimidine oligonucleotide in an acidic buffer solution to form a triple-helix complex. The triple-helix complex is captured with streptavidin-coated magnetic beads. Insert DNA is eluted by adding a pH 9 buffered solution to the captured complex. The purified insert DNA is recovered with a yield of up to 95% and a purity of at least 95%. The isolated insert DNA was directly digested with CviJI restriction endonuclease to generate random fragments for shotgun

sequencing.

L5 ANSWER 29 OF 70 MEDLINE
AN 94077713 MEDLINE
DN 94077713
TI Coincidence painting: a rapid method for cloning region specific DNA sequences [published erratum appears in Nucleic Acids Res 1994 Feb 25;22(4):700].
AU Bailey D M; Carter N P; de Vos D; Leversha M A; Perryman M T; Ferguson-Smith M A
CS Department of Pathology, Cambridge University, UK..
SO NUCLEIC ACIDS RESEARCH, (1993 Nov 11) 21 (22) 5117-23.
Journal code: O8L. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Cancer Journals; Priority Journals
EM 199403
AB We have developed a novel coincidence cloning strategy, termed Coincidence Painting, which enables the rapid generation of large numbers of region specific sequences. Coincidence Painting utilises Degenerate Oligonucleotide Primed PCR (DOP-PCR) amplification of flow sorted derivative translocation chromosomes. The PCR products are hybridised in situ onto specific flow sorted chromosomes for coincident sequence selection. Eluted and reamplified material is then cloned using a novel insert end revelation and ligation technique. Cloned inserts range in size from 150-1300 bps of which approximately 54% appear to be single copy sequences. The cloning method permits the excision of **vector** free probe for library hybridisation screening and the small insert size facilitates analysis for the generation of sequence tagged sites (STSs). We have used such clones successfully for YAC screening by PCR and for **cosmid** screening by filter hybridisation. This new methodology should allow the rapid saturation with probes of regions defined by specific translocation breakpoints.

L5 ANSWER 30 OF 70 MEDLINE
AN 94017232 MEDLINE
DN 94017232
TI Structural analysis of human genome by YAC technologies.
AU Soeda E
SO NIPPON RINSHO. JAPANESE JOURNAL OF CLINICAL MEDICINE, (1993 Sep) 51 (9) 2246-51. Ref: 6
Journal code: KIM. ISSN: 0047-1852.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LA Japanese
EM 199401
AB A method for construction of YAC (**Yeast** Artificial Chromosome) libraries with large inserts has been developed and promoted the ongoing project of human genome. Isolation by PCR screening charges the YAC clone with a unique tag of a pair of PCR primers at the defined chromosome site (Sequence Tagged Sites; STS). Current evaluation of YAC has revealed that larger YAC has more problems where rearrangements including deletion and chimera occur extensively in DNA molecules, presenting a limited use of this technology in mapping; the contig map with mega YACs will be substituted by some other system such as **cosmids** with

which the human healthy and disease genes will be characterized.

```
=> s supercos1

L6            2 SUPERCOS1

=> duplicate remove l6

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n

PROCESSING COMPLETED FOR L6
L7             2 DUPLICATE REMOVE L6 (0 DUPLICATES REMOVED)

=> d 1-2 bib ab


L7   ANSWER 1 OF 2  BIOSIS  COPYRIGHT 1998 BIOSIS
AN   97:109847  BIOSIS
DN   99409050
TI   Construction of ordered overlapping cosmid library and bacterial
     artificial chromosome (BAC) library of Helicobacter pylori.
AU   Ruy B-D; Lee W-K; Cho M-J; Jeon Y-S; Rhee K-H
CS   Dep. Microbiol., Gyeongsang Natl. Univ. Coll. Med., Chinju, Kyung-Nam
     660-280, South Korea
SO   Journal of the Korean Society for Microbiology 31 (5). 1996.
     533-545. ISSN: 0253-3162
LA   Korean
AB   To elucidate the host-parasite relationship on the basis of genome of
     Helicobacter pylori, we constructed a cosmid and a bacterial
     artificial chromosome(BAC) library of Helicobacter pylori isolate
     strain pnd 51. Genomic DNA fragments were cloned into the cosmid
     vector SuperCos1 and a random 868 member library, which
     were 15-fold redundant to Helicobacter pylori genome ( apprx 1700
     kb), were constructed. The cosmids were ordered by dot blot
     hybridization with RNA probes specific for the ends of cloned DNAs.
     Up to now, 34 cosmids were mapped to 8 independent miniset contigs.
     The DNA of each cosmid in the 8 minisets was fingerprinted by
     restriction analysis. The sum of each length of 8 miniset contigs was
     about 810 kb which is considered to cover 48% of the Helicobacter
     pylori genome. A BAC library of Helicobacter pylori genome was also
     constructed to obtain large clones which could facilitate to assembly
     an ordered overlapping library. The genomic DNA of Helicobacter
     pylori was prepared in LMP agarose film, partially digested with Hind
     III and then ligated with pBeloBAC11. We continue to attempt
     transformations of E. coli DH10B/r with these ligates and screenings
     of resultant colonies by in situ colony hybridization. Until now, we
     selected one hundred BAC clones which contained inserts with a range
     of 110 apprx 200 kb in their length.

L7   ANSWER 2 OF 2  MEDLINE
AN   1998050340     MEDLINE
DN   98050340
TI   Construction of Chinese genomic cosmid library.
AU   Qin X; Zhang J; Kong J; Shen Y; Wu G
CS   National Laboratory of Medical Molecular Biology, Institute of Basic
     Medical Sciences, CAMS, Beijing.
SO   CHUNG-KUO I HSUEH KO HSUEH YUAN HSUEH PAO ACTA ACADEMIAE MEDICINAE
     SINICAE, (1996 Oct) 18 (5) 333-7.
     Journal code: CZS. ISSN: 1000-503X.
```

CY China
DT Journal; Article; (JOURNAL ARTICLE)
LA Chinese
EM 199803
EW 19980305
AB A Chinese genomic library has been constructed using **SuperCos1** cosmid vector. 6.09 x 10(5) clones were obtained with an everage insert size of 40 kb ranging from 32 to 45 kb, which cover approximately 8.12 fold human genomic DNA. DNA pools prepared from the total library were screened with 6 known markers distributed on different chromosomes, which all were tested positive.

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	20.26	20.41

STN INTERNATIONAL LOGOFF AT 11:37:03 ON 13 APR 1998

US PAT NO: 5,710,016 [IMAGE AVAILABLE] L1: 1 of 9
DATE ISSUED: Jan. 20, 1998
TITLE: Almond N-glycosidase gene
INVENTOR: Hiroyuki Izu, Kyoto, Japan
Masanori Mitta, Kyoto-fu, Japan
Ikunoshin Kato, Uji, Japan
ASSIGNEE: Takara Shuzo Co., Ltd., Kyoto-fu, Japan (foreign corp.)
APPL-NO: 08/419,009
DATE FILED: Apr. 7, 1995
ART-UNIT: 181
PRIM-EXMR: Keith C. Furman
LEGAL-REP: Browdy and Neimark

US PAT NO: 5,710,016 [IMAGE AVAILABLE] L1: 1 of 9

ABSTRACT:
An almond N-glycosidase gene and genes associated therewith are described. Vectors integrated such genes therein, recombinant microorganisms transformed with said vectors, and a process for preparing the almond N-glycosidase using said recombinant microorganisms are also described.

US PAT NO: 5,686,412 [IMAGE AVAILABLE] L1: 2 of 9
DATE ISSUED: Nov. 11, 1997
TITLE: Protein kinases
INVENTOR: Merl F. Hoekstra, Snohomish, WA
ASSIGNEE: Salk Institute for Biological Studies, La Jolla, CA (U.S. corp.)
APPL-NO: 08/454,097
DATE FILED: May 30, 1995
ART-UNIT: 184
PRIM-EXMR: Robert A. Wax
ASST-EXMR: Gabriele E. Bugaisky
LEGAL-REP: Marshall, O'Toole, Gerstein, Murray & Borun

US PAT NO: 5,686,412 [IMAGE AVAILABLE] L1: 2 of 9

ABSTRACT:
Protein kinase mutant and wild-type genes encoding polypeptides of the class heretofore designated "casein kinase I" and useful in screening compositions which may affect DNA double-strand break repair activity are disclosed. Also disclosed are methods using the polynucleotides in cell-proliferative disorders.

US PAT NO: 5,663,061 [IMAGE AVAILABLE] L1: 3 of 9
DATE ISSUED: Sep. 2, 1997
TITLE: Expression vectors for the synthesis of proteins in the fission yeast schizosaccharomyces pombe
INVENTOR: Michael Broker, Marburg, Federal Republic of Germany
ASSIGNEE: Behringwerke Aktiengesellschaft, Marburg, Federal Republic of Germany (foreign corp.)
APPL-NO: 08/371,576
DATE FILED: Jan. 12, 1995
ART-UNIT: 189
PRIM-EXMR: John LeGuyader
LEGAL-REP: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.

US PAT NO: 5,663,061 [IMAGE AVAILABLE] L1: 3 of 9

ABSTRACT:
Particularly suitable expression vectors for the synthesis of proteins in the fission yeast Schizosaccharomyces pombe (S. pombe) are described. These expression vectors are (in addition to other advantageous elements, equipped with a strong homologous promoter and terminator).

US PAT NO: 5,627,064 [IMAGE AVAILABLE] L1: 4 of 9
DATE ISSUED: May 6, 1997
TITLE: Protein kinases
INVENTOR: Merl F. Hoekstra, Shohomish, WA
ASSIGNEE: The Salk Institute For Biological Studies, La Jolla, CA (U.S. corp.)
APPL-NO: 08/447,500
DATE FILED: May 23, 1995
ART-UNIT: 184
PRIM-EXMR: Robert A. Wax
ASST-EXMR: Gabriele E. Bugaisky
LEGAL-REP: Marshall, O'Toole, Gerstein, Murray & Borun

US PAT NO: 5,627,064 [IMAGE AVAILABLE] L1: 4 of 9

ABSTRACT:
Protein kinase mutant and wild-type genes encoding polypeptides of the class heretofore designated "casein kinase I" and useful in screening compositions which may affect DNA double-strand break repair activity are disclosed. Also disclosed are methods using the polynucleotides in cell-proliferative disorders.

US PAT NO: 5,589,372 [IMAGE AVAILABLE] L1: 5 of 9
DATE ISSUED: Dec. 31, 1996
TITLE: Squalene synthetase
INVENTOR: Gordon W. Robinson, Lawrenceville, NJ
ASSIGNEE: E. R. Squibb & Sons, Inc., Princeton, NJ (U.S. corp.)
APPL-NO: 08/351,981
DATE FILED: Dec. 8, 1994
ART-UNIT: 184
PRIM-EXMR: Robert A. Wax
ASST-EXMR: Eric Grimes
LEGAL-REP: Thomas R. Savitsky, Timothy J. Gaul, James M. Bogden

US PAT NO: 5,589,372 [IMAGE AVAILABLE] L1: 5 of 9

ABSTRACT:
Nucleic acid sequences, particularly DNA sequences, coding for all or part of a squalene synthetase, expression vectors containing the DNA sequences, host cells containing the expression vectors, and methods utilizing these materials. The invention also concerns polypeptide molecules comprising all or part of a squalene synthetase, and methods for producing these polypeptide molecules.

US PAT NO: 5,527,896 [IMAGE AVAILABLE] L1: 6 of 9
DATE ISSUED: Jun. 18, 1996
TITLE: Cloning by complementation and related processes
INVENTOR: Michael H. Wigler, Lloyd Harbor, NY
John J. Colicelli, Los Angeles, CA
ASSIGNEE: Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

(U.S. corp.)
APPL-NO: 07/688,352
DATE FILED: Apr. 19, 1991
ART-UNIT: 187
PRIM-EXMR: Mindy Fleisher
LEGAL-REP: Marshall, O'Toole, Gerstein, Murray & Borun

US PAT NO: 5,527,896 [IMAGE AVAILABLE] L1: 6 of 9

ABSTRACT:
Disclosed are methods for detecting mammalian genes encoding proteins which can function in microorganisms, particularly yeast, to modify, complement, or suppress a genetic defect associated with an identifiable phenotypic alteration or characteristic in the microorganism. Disclosed also are mammalian DNA sequences cloned by the above method, as well as polypeptide products of the expression of the DNA sequences in procaryotic or eucaryotic host cells and antibody substances which are specifically immunoreactive with said expression products. More specifically, the present invention relates to methods for cloning mammalian genes which encode products which modify, complement or suppress a genetic defect in a biochemical pathway in which cAMP participates or in a biochemical pathway which is controlled, directly or indirectly, by a RAS-related protein, to products (RNA, proteins) encoded by the mammalian genes cloned in this manner, and to antibodies which can bind the encoded proteins.

US PAT NO: 5,443,962 [IMAGE AVAILABLE] L1: 7 of 9
DATE ISSUED: Aug. 22, 1995
TITLE: Methods of identifying inhibitors of cdc25 phosphatase
INVENTOR: Giulio Draetta, Winchester, MA
Guillaume Cottarel, Chestnut Hill, MA
Veronique Damagnez, Cambridge, MA
ASSIGNEE: Mitotix, Inc., Cambridge, MA (U.S. corp.)
APPL-NO: 08/073,383
DATE FILED: Jun. 4, 1993
ART-UNIT: 184
PRIM-EXMR: Robert A. Wax
ASST-EXMR: Eric Grimes
LEGAL-REP: Matthew P. Vincent, Giulio A.Lahive & Cockfield DeConti, Jr.

US PAT NO: 5,443,962 [IMAGE AVAILABLE] L1: 7 of 9

ABSTRACT:
The present invention makes available assays and reagents for identifying anti-proliferative agents, such as mitotic and meiotic inhibitors, especially inhibitors of cdc25 phosphatase. The present assay provides a simple and rapid screening test which relies on scoring for positive cellular proliferation as indicative of anti-mitotic or anti-meiotic activity, and comprises contacting a candidate agent with a cell which has an impaired cell-cycle checkpoint and measuring the level of proliferation in the presence and absence of the agent. The checkpoint impairment is such that it either causes premature progression of the cell through at least a portion of a cell-cycle or inhibition of normal progression of the cell through at least a portion of a cell-cycle, but can be off-set by the action of an agent which inhibits at least one regulatory protein of the cell-cycle in a manner which counter-balances the effect of the impairment.

US PAT NO: 5,441,880 [IMAGE AVAILABLE] L1: 8 of 9
DATE ISSUED: Aug. 15, 1995
TITLE: Human cdc25 genes, encoded products and uses thereof
INVENTOR: David H. Beach, Huntington Bay, NY
Konstantin Galaktionov, Cold Spring Harbor, NY
ASSIGNEE: Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (U.S. corp.)
APPL-NO: 08/124,569
DATE FILED: Sep. 20, 1993
ART-UNIT: 184
PRIM-EXMR: Keith C. Furman
ASST-EXMR: Hyosuk Kim
LEGAL-REP: Matthew P. Vincent, Giulio A.Lahive & Cockfield DeConti, Jr.

US PAT NO: 5,441,880 [IMAGE AVAILABLE] L1: 8 of 9

ABSTRACT:
Two previously undescribed human cdc25 genes, designated cdc25 A and cdc25 B, which have been shown to have an endogenous tyrosine phosphatase activity that can be specifically activated by B-type cyclin, in the complete absence of cdc2.
As a result of the work described herein, new approaches to regulating the cell cycle in eukaryotic cells and, particularly, to regulating the activity of tyrosine specific phosphatases which play a key role in the cell cycle are available. Applicant's invention relates to methods of regulating the cell cycle and, specifically, to regulating activation of cdc2-kinase, through alteration of the activity and/or levels of tyrosine phosphatases, particularly cdc25 phosphatase, and B-type cyclin or through alteration of the interaction of components of MPF, particularly the association of cdc25 with cyclin, cdc2 or the cdc2/cyclin B complex. The present invention also relates to agents or compositions useful in the method of regulating (inhibiting or enhancing) the cell cycle. Such agents or compositions are, for example, inhibitors (such as low molecular weight peptides or compounds, either organic or inorganic) of the catalytic activity of tyrosine specific PTPases (particularly cdc25), blocking agents which interfere with interaction or binding of the tyrosine specific PTPase with cyclin or the cyclin/cdc2 complex, or agents which interfere directly with the catalytic activity of the PTPases.

US PAT NO: 5,270,201 [IMAGE AVAILABLE] L1: 9 of 9
DATE ISSUED: Dec. 14, 1993
TITLE: Artificial chromosome vector
INVENTOR: Eric J. Richards, Lloyd Harbor, NY
Frederick M. Ausubel, Newton, MA
ASSIGNEE: The General Hospital Corporation, Boston, MA (U.S. corp.)
APPL-NO: 07/860,585
DATE FILED: Mar. 30, 1992
ART-UNIT: 185
PRIM-EXMR: Richard A. Schwartz
ASST-EXMR: Philip W. Carter
LEGAL-REP: Sterne, Kessler, Goldstein & Fox

US PAT NO: 5,270,201 [IMAGE AVAILABLE] L1: 9 of 9

ABSTRACT:
The present invention relates to a recombinant DNA molecule which

contains the telomere and, optionally, the centromere of a higher eukaryote, particularly a plant, the telomere itself, the centromere itself, a method of producing a polypeptide in a recipient cell which utilizes said recombinant DNA molecule, host cells transformed with said recombinant molecule, and uses for said recombinant molecule.

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y

U.S. Patent & Trademark Office LOGOFF AT 16:11:43 ON 13 APR 1998

Search Paper 3

```
Trying 11180...Open

PLEASE ENTER HOST PORT ID:
PLEASE ENTER HOST PORT ID:x
LOGINID:d185jsb
PASSWORD:
TERMINAL (ENTER 1, 2, 3, 4, OR ?): 3


  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *                                                               *
  *           Welcome to MESSENGER (APS Text) at USPTO            *
  *                                                               *
  *                                                               *
  *    The USPTO production files are current through:            *
  *    APR 07 1998 for U.S. Patent Text Data.                     *
  *    APR 07 1998 for U.S. Current Classification data.          *
  *    APR 07 1998 for U.S. Patent Image Data.                    *
  *                                                               *
  *       * PLEASE USE 305-9000 FOR NEW TELEPHONE NUMBER *        *
  *                                                               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  * More U.S. patent data is now available on APS.  The new       *
  * USOCR file contains patents issued in 1970, plus some         *
  * patents that were missing from the USPAT file.  See the       *
  * Patents News Folder under the Public Folders in e-mail for    *
  * more information on using the new file.  Thank you.           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *  DISCLAIMER:                                                  *
  *  Neither the United States Government, nor any agency         *
  *  thereof, nor any of their contractors, subcontractors or     *
  *  employees make any warranty, expressed or implied,           *
  *  including any warranty of marketability of fitness for a     *
  *  particular purpose; nor assumes any legal liability or       *
  *  responsibility for any party's use, or the results of        *
  *  such, of the data.                                           *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *                Help Desk --> 703-305-9000                     *
  *                                                               *
  *    The Help Desk is staffed for APS support 7 days/week.      *
  *      Monday through Friday:      6:30am - 9:00pm              *
  *      Saturday, Sunday, Holidays: 8:30am - 5:00 pm             *
  *                                                               *
  *    The Help Desk staff at this number will handle all APS     *
  *    related questions.                                         *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *    >>>>>>>>>>>>> NEW SUNDAY HOURS !!! <<<<<<<<<<<<<           *
  *                                                               *
  *    The APS is available:                                      *
  *            6:30am - 9:00pm Monday through Friday              *
  *            7:30am - 5:00pm Saturday, Sunday, Holidays         *
  *                                                               *
  *      APS is unavailable Thanksgiving Day, Christmas Day,      *
  *      and New Year's Day.                                      *
  *                                                               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
FILE 'USPAT' ENTERED AT 15:48:19 ON 13 APR 1998

  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *              W E L C O M E   T O   T H E                      *
```

indicate that the origin recognition machinery is conserved across species, since the same OBR region functions in both Syrian and Chinese hamster cells. Importantly, while cCAD1 exhibits characteristics of a complete replicon, we have not detected **autonomous** replication directly following transfection. Since the CAD episome was generated after excision of chromosomally integrated transfected cCAD1 sequences, we propose that prior localization within a chromosome may be necessary to "license" some biochemically defined OBRs to render them functional.

L6 ANSWER 7 OF 26 MEDLINE
AN 95249551 MEDLINE
DN 95249551
TI A prokaryotic origin for light-dependent chlorophyll biosynthesis of plants.
AU Suzuki J Y; Bauer C E
CS Department of Biology, Indiana University, Bloomington 47405, USA..
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1995 Apr 25) 92 (9) 3749-53.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-L37783
EM 199508
AB Flowering plants require light for chlorophyll synthesis. Early studies indicated that the dependence on light for greening stemmed in part from the light-dependent reduction of the chlorophyll intermediate protochlorophyllide to the product chlorophyllide. Light-dependent reduction of protochlorophyllide by flowering plants is contrasted by the ability of nonflowering plants, algae, and photosynthetic bacteria to reduce protochlorophyllide and, hence, synthesize (bacterio) chlorophyll in the dark. In this report, we functionally complemented a light-independent protochlorophyllide reductase mutant of the eubacterium Rhodobacter capsulatus with an expression library composed of genomic DNA from the cyanobacterium Synechocystis sp. PCC 6803. The complemented R. capsulatus strain is capable of synthesizing bacteriochlorophyll in the light, thereby indicating that a chlorophyll biosynthesis enzyme can function in the bacteriochlorophyll biosynthetic pathway. However, under dark growth conditions the complemented R. capsulatus strain fails to synthesize bacteriochlorophyll and instead accumulates protochlorophyllide. Sequence analysis demonstrates that the complementing Synechocystis genomic DNA fragment exhibits a high degree of sequence identity (53-56%) with light-dependent protochlorophyllide reductase enzymes found in plants. The observation that a plant-type, light-dependent protochlorophyllide reductase enzyme exists in a cyanobacterium indicates that light-dependent protochlorophyllide reductase evolved before the advent of eukaryotic photosynthesis. As such, this enzyme did not arise to fulfill a function necessitated either by the endosymbiotic evolution of the chloroplast or by multicellularity; rather, it evolved to fulfill a fundamentally cell-**autonomous** role.

L6 ANSWER 8 OF 26 MEDLINE
AN 96021609 MEDLINE
DN 96021609
TI A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.

AU Zumstein E; Pearson B M; Kalogeropoulos A; Schweizer M
CS Institute of Food Research, Genetics & Microbiology Department, Norwich Research Park, Colney, U.K.
SO YEAST, (1995 Aug) 11 (10) 975-86.
Journal code: YEA. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X83121; GENBANK-M73270
EM 199604
AB The nucleotide sequence of a 29.425 kb fragment localized on the left arm of chromosome XV from Saccharomyces cerevisiae has been determined. The sequence contains 13 open reading frames (ORFs) of which four encode the known genes ADH1, COQ3, MSH2 and RCF4. Predictions are made concerning the functions of the unknown ORFs. Some of the ORFs contain sequences similar to expressed sequence tags (EST) found in the database made available by TIGR. In particular, the highly expressed ADH1 gene is represented in this database by no less than 20 EST sequences. Two **ARS** sequences and a putative functional GCN4 motif have also been detected. One ORF (O0953) containing nine putative transmembrane segments is similar to a hypothetical membrane protein of Arabidopsis thaliana. Characteristic features of the other ORFs include ATP/GTP binding sites, a fungal Zn(2)-Cys(6) binuclear centre, an endoplasmic reticulum targeting sequence, a beta-transducin repeat signature and in two instances, good similarity to the prokaryotic lipoprotein signal peptide motif.

L6 ANSWER 9 OF 26 MEDLINE
AN 95112788 MEDLINE
DN 95112788
TI Complete DNA sequence of yeast chromosome II.
AU Feldmann H; Aigle M; Aljinovic G; Andre B; Baclet M C; Barthe C; Baur A; Becam A M; Biteau N; Boles E; et al
CS Institut fur Physiologische Chemie, Physikalische Biochemie und Zellbiologie, Universitat Munchen, Germany..
SO EMBO JOURNAL, (1994 Dec 15) 13 (24) 5795-809.
Journal code: EMB. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-Z35762; GENBANK-Z35763; GENBANK-Z35764; GENBANK-Z35765; GENBANK-Z35766; GENBANK-Z35767; GENBANK-Z35768; GENBANK-Z35769; GENBANK-Z35770; GENBANK-Z35771; GENBANK-Z35773; GENBANK-Z35774; GENBANK-Z35775; GENBANK-Z35776; GENBANK-Z35777; GENBANK-Z35778; GENBANK-Z35779; GENBANK-Z35780; GENBANK-Z35781; GENBANK-Z35782; GENBANK-Z35783; GENBANK-Z35784; GENBANK-Z35785; GENBANK-Z35786; GENBANK-Z35787; GENBANK-Z35788; GENBANK-Z35789; GENBANK-Z35790; GENBANK-Z35791; GENBANK-Z35792
EM 199504
AB In the framework of the EU genome-sequencing programmes, the complete DNA sequence of the yeast Saccharomyces cerevisiae chromosome II (807 188 bp) has been determined. At present, this is the largest eukaryotic chromosome entirely sequenced. A total of 410 open reading frames (ORFs) were identified, covering 72% of the sequence. Similarity searches revealed that 124 ORFs (30%) correspond to genes of known function, 51 ORFs (12.5%) appear to be homologues of genes whose functions are known, 52 others (12.5%)

have homologues the functions of which are not well defined and another 33 of the novel putative genes (8%) exhibit a degree of similarity which is insufficient to confidently assign function. Of the genes on chromosome II, 37-45% are thus of unpredicted function. Among the novel putative genes, we found several that are related to genes that perform differentiated functions in multicellular organisms of are involved in malignancy. In addition to a compact arrangement of potential protein coding sequences, the analysis of this chromosome confirmed general chromosome patterns but also revealed particular novel features of chromosomal organization. Alternating regional variations in average base composition correlate with variations in local gene density along chromosome II, as observed in chromosomes XI and III. We propose that functional **ARS** elements are preferably located in the AT-rich regions that have a spacing of approximately 110 kb. Similarly, the 13 tRNA genes and the three Ty elements of chromosome II are found in AT-rich regions. In chromosome II, the distribution of coding sequences between the two strands is biased, with a ratio of 1.3:1. An interesting aspect regarding the evolution of the eukaryotic genome is the finding that chromosome II has a high degree of internal genetic redundancy, amounting to 16% of the coding capacity.

L6 ANSWER 10 OF 26 MEDLINE DUPLICATE 6
AN 94357432 MEDLINE
DN 94357432
TI Characterization of an efficient gene cloning strategy for Aspergillus niger based on an **autonomously** replicating plasmid: cloning of the nicB gene of A. niger.
AU Verdoes J C; Punt P J; van der Berg P; Debets F; Stouthamer A H; van den Hondel C A
CS Department of Molecular Genetics and Gene Technology, TNO Nutrition and Food Research Institute, Rijswijk, The Netherlands..
SO GENE, (1994 Sep 2) 146 (2) 159-65.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199412
AB The development of an improved gene cloning strategy by complementation of mutant alleles in Aspergillus niger is described. The strategy is based on the use of a fungal **autonomously** replicating vector, pAB4-ARp1. This vector was constructed by the introduction of a previously described sequence involved in **autonomous** replication (AMA1), into a pyrG integrative vector, pAB4-1. With vector pAB4-ARp1, a 10-100-fold increase in transformation frequency was obtained, as compared to pAB4-1. Furthermore, the transformation frequency of a co-transformed plasmid is also increased using pAB4-ARp1. A. niger transformants containing pAB4-ARp1 are mitotically unstable. Co-transformed plasmids strictly co-segregated with the **autonomously** replicating vector, as a result of recombination between both vectors. The use of pAB4-ARp1 in gene cloning was demonstrated by the complementation of two linkage group-VII-specific A. niger mutants. Complementation of a lysF mutant was achieved by co-transformation of pAB4-ARp1 with total genomic A. niger DNA ('instant bank'). A nicB-deficient A. niger was complemented by co-transformation with pAB4-ARp1 and an A. niger **cosmid** library. The complementing DNA was re-isolated from a Nic+